

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2004, 21:27:04 ; Search time 23 Seconds
(without alignments)
965.181 Million cell updates/sec

Title: US-09-700-696C-2
Perfect score: 2279
Sequence: 1 VNKEXISNKENTHNGLRMS.....RADDSESGSGSSGSDGD 430

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued.Patente_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCUTS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/Deckfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	2276	99.9	525	4	US-10-132-920B-27 Sequence 27, Appl
2	2157	94.6	430	4	US-10-132-920B-2 Sequence 2, Appl
3	140	6.1	772	1	US-08-524-757-12 Sequence 12, Appl
4	136	6.0	1187	1	US-08-320-559-28 Sequence 28, Appl
5	136	6.0	1187	3	US-08-545-860D-28 Sequence 28, Appl
6	136	6.0	1187	5	PCT-US94-0496-28 Sequence 28, Appl
7	136	6.0	1210	1	US-08-320-559-26 Sequence 26, Appl
8	136	6.0	1210	3	US-08-545-860D-26 Sequence 26, Appl
9	136	6.0	1210	5	PCT-US94-0496-26 Sequence 26, Appl
10	135.5	5.9	723	1	US-07-814-964-11 Sequence 11, Appl
11	135.5	5.9	723	1	US-08-258-442-11 Sequence 11, Appl
12	135.5	5.9	723	1	US-08-328-809-6 Sequence 6, Appl
13	135.5	5.9	723	4	US-08-866-840-6 Sequence 6, Appl
14	135.5	5.9	723	5	PCT-US92-1107-11 Sequence 11, Appl
15	135	5.9	1742	4	US-09-386-962C-4 Sequence 4, Appl
16	134.5	5.9	1115	2	US-08-568-459A-2 Sequence 2, Appl
17	134.5	5.9	1115	2	US-08-487-826B-2 Sequence 2, Appl
18	134.5	5.9	1115	4	US-09-210-288-2 Sequence 2, Appl
19	134.5	5.9	1115	6	5198347-6 Patent No. 5198347
20	128	5.6	703	3	US-08-910-925-4 Sequence 4, Appl
21	127.5	5.6	1235	1	US-08-118-101A-2 Sequence 2, Appl
22	126.5	5.6	455	5	PCT-US93-07261-13 Sequence 13, Appl
23	126.5	5.6	1663	5	PCT-US93-07261-16 Sequence 16, Appl
24	125.5	5.5	1261	3	US-09-208-742-4 Sequence 4, Appl
25	125.5	5.5	1261	4	US-09-332-295-2 Sequence 2, Appl
26	125.5	5.5	1261	4	US-09-709-979-2 Sequence 2, Appl
27	125.5	5.5	1261	4	US-10-147-268-2 Sequence 2, Appl

28	124.5	5.5	1183 4	US-09-134-001C-3530 Sequence 3530, Ap
29	123	5.4	493 3	US-08-999-774A-12 Sequence 12, Appl
30	123	5.4	1177 5	US-09-134-001C-5106 Sequence 5106, Ap
31	123	5.4	1588 4	PCT-US93-07261-11 Sequence 11, Appl
32	122	5.4	690 4	US-09-134-001C-4568 Sequence 4568, Ap
33	121.5	5.3	754 4	US-09-976-594-375 Sequence 375, Ap
34	121	5.3	1404 4	US-08-801-308-1 Sequence 1, Appl
35	120.5	5.3	1435 2	US-08-568-459A-4 Sequence 4, Appl
36	120.5	5.3	1435 2	US-08-487-826B-4 Sequence 4, Appl
37	120.5	5.3	1250 4	US-09-210-288-4 Sequence 4, Appl
38	120	5.3	1250 4	US-08-441-139-9 Sequence 9, Appl
39	120	5.3	2842 1	US-07-741-940-7 Sequence 7, Appl
40	120	5.3	2842 1	US-08-289-548A-7 Sequence 7, Appl
41	120	5.3	2842 1	US-08-452-654-7 Sequence 7, Appl
42	120	5.3	2842 4	US-08-449-731-7 Sequence 7, Appl
43	120	5.3	2843 1	US-07-741-940-2 Sequence 2, Appl
44	120	5.3	2843 1	US-08-289-548A-2 Sequence 2, Appl
45	120	5.3	2843 1	US-08-452-654-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-132-920B-27
Sequence 27, Application US/10132920B
Patent No. 6673900
GENERAL INFORMATION:
APPLICANT: Rowe, Peter
TITLE OF INVENTION: A Polypeptide Hormone-Phosphatonic
FILE REFERENCE: BEAR-0050CN
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 09/434,185
PRIOR FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapien
US-10-132-920B-27

Query Match 99.9%; Score 2276; DB 4; Length 525;
Best Local Similarity 99.8%; Pred. No. 1.3e-186;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	VNKEXISNKENTHNGLRMSIYPKSTGNKGFEDGDALSKLHDOEYGAALIRNNOHIM	60
DB	96	LNKEXISNKENTHNGLRMSIYPKSTGNKGFEDGDALSKLHDOEYGAALIRNNOHIM	155
QY	61	GPVTAIKLIGENKENTPNVNIIPASMTYAKASDKKKKQPDSDCAQKSPVSKSTHR	120
DB	156	GPVTAIKLIGENKENTPNVNIIPASMTYAKASDKKKKQPDSDCAQKSPVSKSTHR	215
QY	121	IQHNIDYIKLISKVKKIPSDPFGSGYTDIOERGNDISPFSGDQPFKDIPKGGATGPD	180
DB	216	IQHNIDYIKLISKVKKIPSDPFGSGYTDIOERGNDISPFSGDQPFKDIPKGGATGPD	275
QY	181	LEKQDQTFAGSEASESTHLDTKKPGVNEIEREENGANTIGTDETAKEADAVSVLY	240
DB	276	LEKQDQTFAGSEASESTHLDTKKPGVNEIEREENGANTIGTDETAKEADAVSVLY	335
QY	241	EGSNDIMSGTNEKELPREGNRVDAGSONAHQKVEFYHPAPSKKREKSGSDAASFN	300
DB	336	EGSNDIMSGTNEKELPREGNRVDAGSONAHQKVEFYHPAPSKKREKSGSDAASFN	395
QY	301	YNELPKQKSTKTKGVDSNRNOATLNEKORPFSKSKSGGLPSPHGLNNEIKNEADSFN	360
DB	396	YNELPKQKSTKTKGVDSNRNOATLNEKORPFSKSKSGGLPSPHGLNNEIKNEADSFN	455
QY	361	GPSHENITTHGRKYVYPPHRRNNSTNKKMPQCKSGWGQPHSNRPFSRRRDSSESD	420

Db 456 GPHENITTHGRKHYVPHRQNNSTNNKGMPOGKSWGRPHSNRRFSSRRDDSSSD 515
 QY 421 SSSSSSDGD 430
 Db 516 SSSSSSDGD 525

RESULT 2

US-10-132-920B-2
 ; Sequence 2, Application US/10132920B
 ; Patent No. 6673900
 ; GENERAL INFORMATION:
 ; APPLICANT: Rowe, Peter
 ; TITLE OF INVENTION: A Polypeptide Hormone-Phosphatoinh
 ; FILE REFERENCE: BEAR-005CON
 ; CURRENT APPLICATION NUMBER: US/10/132,920B
 ; PRIOR FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: 09/434,185
 ; NUMBER OF SEQ ID NOS: 55
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 430
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-10-132-920B-2

Query Match 94.6%; Score 2157; DB 4; Length 430;
 Best Local Similarity 92.8%; Pred. No. 1.5e-176;
 Matches 414; Conservative 0; Mismatches 0; Indels 32; Gaps 2;

QY 1 VNKEYSINKENTNGLKMSIYPTKSTGKGFEDDDAISKLHDEEYGAALIRNMQHIM 60
 Db 1 VNKEYSINKENTNGLKMSIYPTKSTGKGFEDDDAISKLHDEEYGAALIRNMQHIM 60
 QY 61 GPVTAIKLGEENKENTPRVLTNIIPASMYAKAKSKDKKPPORDSOAKSPVSKSTHR 120
 Db 61 GPVTAIKLGEENKENTPRVLTNIIPASMYAKAKSKDKKPPORDSOAKSPVSKSTHR 120
 QY 121 IQHNIDYIKHLKSKVKKIPSPDEGSGYTDLOERGNDISPF-----SGDG 164
 Db 121 IQHNIDYIKHLKSKVKKIPSPDEGSGYTDLOERGNDISPF-----SGDG 164
 QY 121 IQHNIDYIKHLKSKVKKIPSPDEGSGYTDLOERGNDISPF-----SGDG 180
 Db 121 IQHNIDYIKHLKSKVKKIPSPDEGSGYTDLOERGNDISPF-----SGDG 180
 QY 165 QPFCIKPKGKATGPDLEGKDIQTGFAPSEASTHLDTKPKGYNEIPEREENGANTIGT 224
 Db 165 QPFCIKPKGKATGPDLEGKDIQTGFAPSEASTHLDTKPKGYNEIPEREENGANTIGT 224
 QY 181 QPFCIKPKGKATGPDLEGKDIQTGFAPSEASTHLDTKPKGYNEIPEREENGANTIGT 224
 Db 181 QPFCIKPKGKATGPDLEGKDIQTGFAPSEASTHLDTKPKGYNEIPEREENGANTIGT 224
 QY 225 RDETAKEADAVDVSLVEGSDIMGSTNFKELPGREGNVDAGSQNAHQGKVEFYPPAPS 284
 Db 225 RDETAKEADAVDVSLVEGSDIMGSTNFKELPGREGNVDAGSQNAHQGKVEFYPPAPS 284
 QY 285 KEKKEGSDAESTNNYNEIPKMGKSTRKGVDSNRNQAATLNEKQRPSPKSGQGLPIP 344
 Db 285 KEKKEGSDAESTNNYNEIPKMGKSTRKGVDSNRNQAATLNEKQRPSPKSGQGLPIP 344
 QY 345 SRGLDNEIKNEMDSFNGPSHENITTHGRKHYVPHRQNNSTNNKGMPOGKSWGRPHSN 404
 Db 345 SRGLDNEIKNEMDSFNGPSHENITTHGRKHYVPHRQNNSTNNKGMPOGKSWGRPHSN 404
 QY 405 RFPSSRRDDSSSDSGSSSDGD 430
 Db 405 RFPSSRRDDSSSDSGSSSDGD 430

RESULT 3

US-08-524-757-12
 ; Sequence 12, Application US/08524757
 ; Patent No. 5792634
 ; GENERAL INFORMATION:
 ; APPLICANT: Conaway, Ronald C.
 ; APPLICANT: Conaway, Joan W.
 ; APPLICANT: Bradsher, John N.
 ; TITLE OF INVENTION: RNA Polymerase Transcription Factor

NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
 STREET: 1201 Elm Street, Suite 4500
 CITY: Dallas
 STATE: TX
 COUNTRY: US
 ZIP: 75270-2197
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/524,757
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/13621
 FILING DATE: 29-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/160087
 FILING DATE: 30-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Hatte, John A.
 REGISTRATION NUMBER: 37,345
 REFERENCE/DOCKET NUMBER: B35006CIPCIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (214) 939-4500
 TELEFAX: (214) 939-4600
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 772 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; US-08-524-757-12

Query Match 6.1%; Score 140; DB 1; Length 772;
 Best Local Similarity 20.5%; Pred. No. 0.0017;
 Matches 87; Conservative 49; Mismatches 144; Indels 144; Gaps 17;

QY 23 PKSTNGKGFEDDDAISKLHDEEYGAALIRNMQHIMGPVTAIKLGEENKENTPRVLT 82
 Db 210 PKGHSNAPQDLRGLASQERHLGEPRGKGVSONKER----- 245
 QY 83 NIIPASMYAKAKSKDKKPPORDSOAKSPVSKSTHRIQHNIDYIKHLKSKVKKIPSPDE 142
 Db 246 -----KSHDKRVDKAKDEKASVVSREKSH-----KALSK----- 277
 QY 143 GSGYTDLOERGNDISPFSGDQPPKDIIPKGEATGPDLEKDIQTGFAPSEASTHL 201
 Db 278 -----EENRPPSGDNAREKP--PSSGVKKEKREGLSKKCLPSEASDNL 325
 QY 202 DTKPKGYNEIPEREENGANTIGRDETAKEADAVDVSLVEGSDIM-----GSTNFKEL 255
 Db 326 --KKEPHRD--PEKAK-----LDKSKGGLDSFDTG--KAGDILLPKYKKGSLNLT 372
 QY 256 PREGNVDAGSQNAHQGY-----EFHYV-----PAPSKKKEGSDAAS 298
 Db 373 EGVKTNLDRKSLGS--LPKVEETDMEDEFEQPTMSFEESYLSYDQPKKKKIVKT-SATA 430
 QY 299 TYNNEIPKMGKSTRKGVDSNRNQAATLNEKQRPSPKSGQGL----- 341
 Db 431 LGDKGLKNDKSTGKGLDSVQGLPKVNTKSEKPRGADLAKLRKVPDVLPTLPDLPLPA 490
 QY 342 -----PIPSRGDNEIKNEMDSFNGPSHEN-----ITTHGRKHYVP----- 378
 Db 491 IQANYRPLPLBELISSFQPKRAKFSBPQEEBAGFTGRMMNMQVYSGSKCAYLPKXMT 550
 QY 379 -HRQ 381
 Db 551 LHOQ 554

RESULT 4

US-08-320-559-28
Sequence 28, Application US/08320559
Patent No. 5633135

GENERAL INFORMATION:

APPLICANT: Croce, Carlo
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
TITLE OF INVENTION: All-1 Region
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,559
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-OCT-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0855
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO. 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-320-559-28

Query Match 6.0%; Score 136; DB 1; Length 1187;
Best Local Similarity 20.6%; Pred. No. 0.007;

Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

QY 92 AKASHKDKKKKPPORDS-----QACKSPVSKSTHRIQINIDYLKHLSTVK 135
DB 530 SEHSESKDPPKSSSKAPRAPEAPHGKSCQSPAQGPBPQQTGTQPK-----K 584
QY 136 KIPSPFEGSGYTDLCERGNDNISPFSGGQPFKDI-----GKGE-----ATGPD 181
DB 585 PVKASAPARAGSRISLQGEREPGLPYGSRDQTSKDKPKVTKGRPRMAASNEPKPAVPS 644
QY 182 ECKDIQTGPAGSSEAS-----THDTPKKPGY-----NEIPEREENGANTIGTDE 227
DB 645 EKKKKHKSILPAPSKALSGPEPAKDNVEDTPEHFLVPLTESQGFPHSGSGSRISGCGQA 704

RESULT 5

US-08-545-860D-28
Sequence 28, Application US/08545860D
Patent No. 6040140

GENERAL INFORMATION:

APPLICANT: Croce, Carlo
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,860D
FILING DATE: 07-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10930
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/327,392
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,443
FILING DATE: 14-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,094
FILING DATE: 30-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,839
FILING DATE: 27-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,093
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Deluca Esq., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1262

QY 228 TAKEADAVDVLVSGSNDIMGSTNFKELPGRBNRY-----DAGSQNAHQKVE 276
DB 705 VVQEDSKDRPLPLPDLTKLSPLRDPPEPQSLMKITDLSRLTPQPPKSGSRQKAE 764
QY 277 FHYPPAPSKERKKGSSDAESTNYNEIPKNGKSTKGYVDSNRNATLNEKORPFSKG 336
DB 765 DKOPPAGKHSSEKSSDS-----SKLAKRKGEARDCC-----NKKLR----- 805
QY 337 KSGGLPIPSRLDNEIKNEMDSFNGSPHENIT-----HGKHYVPHRONSTRNK 388
DB 806 -----LEKIKSQSSSSSSSHKSKXTKPSRPSQSSKXKLLPPPVSSSSQK 854
QY 389 GMPQKGS-----WGRQF-----HSNRFRSSRRDDSSSSSSSSSE---SDQ 430
DB 855 AKPALKRRBRADTCGQPPKASASTKSNHRDSSIPQORVYEGKGRSSSEHKSSGD 912

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1187 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-545-860D-28

Query Match 6.0%; Score 136; DB 3; Length 1187;
 Best Local Similarity 20.6%; Pred. No. 0.007;

Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

QY 92 AKAHKDKKKKQKRS-----QAQSPVKSSTHRIQHNDILKLSKV 135
 DB 530 SQEHSEKRDPPKSSSKAPAPAPAPAPKRSCKSPQDEPPQRTVTGKPK-----K 584
 QY 136 KIPDFEGSGYTDLQERGDNDISPFSGDGPFPDIP---GKGE-----ATGPD 181
 DB 585 PVKASARAAGSTSLQGEREPGLPYGSRDQTSKDKPKVTKGRPRAAASNEPKPAVPSS 644
 QY 182 EKKDIQTGFAGPSSAES-----THLDTKKRGY-----NEIPREENGNTIGTRDE 227
 DB 645 EKKHKSSLPAPSKALSGPEPAKDNVEDRTEHPALVPLTESQGPFSHSGSRTSGCKQA 704
 QY 228 TAKADAVDVSLVSGNDIMGSTNFKELPREGNRV-----DAGSONAHQKVE 276
 DB 705 VVVOEDSKRDLPLRLDTKLSLPLRDTPPQSLMVKITLTLRIIPQPKGSRQRAE 764
 QY 277 FHYPAPEKREKKGSSDAESTVNEIPKXGKSTKRGVHSNRQATLNEKQRPFGK 336
 DB 765 DKQPPAGKHSEKSSDS-----SKLAKRKGAEARDCD-----NKXIR----- 805
 QY 337 KSGGLPIRGLDNEIKNEMDSFNGPSHENIT-----HGKRYVYVPHRONSTENK 388
 DB 806 -----LEKIKQSSSSSSSHKESKTPSPRSSSSSKKEMLPPEPVSSSSQKP 854
 QY 389 GMPQKGS-----WGRQ-----HSNRPFSSRRDDSSSSSSSSSSS---SDGD 430
 DB 855 AKPALKRSRREADTGCDPPKASSTKSNHSDSIPKQRYVEGKSSSSSHKSSGSD 912

RESULT 6
 PCT-US94-04496-28
 Sequence 28, Application PC/TUS9404496
 GENERAL INFORMATION:
 APPLICANT: Croce, Carlo
 APPLICANT: Canaan, Eli
 TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
 TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
 TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
 NUMBER OF SEQUENCES: 86
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
 ADDRESS: Norris
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04496
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Deluca Esq., Mark

REGISTRATION NUMBER: 33,229
 REFERENCE/DOCKET NUMBER: TJU-1242
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1187 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US94-04496-28

Query Match 6.0%; Score 136; DB 5; Length 1187;
 Best Local Similarity 20.6%; Pred. No. 0.007;

Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

QY 92 AKAHKDKKKKQKRS-----QAQSPVKSSTHRIQHNDILKLSKV 135
 DB 530 SQEHSEKRDPPKSSSKAPAPAPAPAPKRSCKSPQDEPPQRTVTGKPK-----K 584
 QY 136 KIPDFEGSGYTDLQERGDNDISPFSGDGPFPDIP---GKGE-----ATGPD 181
 DB 585 PVKASARAAGSTSLQGEREPGLPYGSRDQTSKDKPKVTKGRPRAAASNEPKPAVPSS 644
 QY 182 EKKDIQTGFAGPSSAES-----THLDTKKRGY-----NEIPREENGNTIGTRDE 227
 DB 645 EKKHKSSLPAPSKALSGPEPAKDNVEDRTEHPALVPLTESQGPFSHSGSRTSGCKQA 704
 QY 228 TAKADAVDVSLVSGNDIMGSTNFKELPREGNRV-----DAGSONAHQKVE 276
 DB 705 VVVOEDSKRDLPLRLDTKLSLPLRDTPPQSLMVKITLTLRIIPQPKGSRQRAE 764
 QY 277 FHYPAPEKREKKGSSDAESTVNEIPKXGKSTKRGVHSNRQATLNEKQRPFGK 336
 DB 765 DKQPPAGKHSEKSSDS-----SKLAKRKGAEARDCD-----NKXIR----- 805
 QY 337 KSGGLPIRGLDNEIKNEMDSFNGPSHENIT-----HGKRYVYVPHRONSTENK 388
 DB 806 -----LEKIKQSSSSSSSHKESKTPSPRSSSSSKKEMLPPEPVSSSSQKP 854
 QY 389 GMPQKGS-----WGRQ-----HSNRPFSSRRDDSSSSSSSSSSS---SDGD 430
 DB 855 AKPALKRSRREADTGCDPPKASSTKSNHSDSIPKQRYVEGKSSSSSHKSSGSD 912

RESULT 7
 US-08-520-559-26
 Sequence 26, Application US/08320559
 Patent No. 5631135
 GENERAL INFORMATION:
 APPLICANT: Croce, Carlo
 APPLICANT: Canaan, Eli
 TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
 TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
 TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
 TITLE OF INVENTION: All-1 Region
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5631135
 ADDRESS: Norris
 STREET: One Liberty Place - 46th floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/320,559
 FILING DATE:

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/062,443
 FILING DATE: 14 MAY 1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/971,094
 FILING DATE: 30-OCT-92
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/888,830
 FILING DATE: 27-MAY-92
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/805,093
 FILING DATE: 11-DEC-91
 ATTORNEY/AGENT INFORMATION:
 NAME: Deluca, Mark
 REGISTRATION NUMBER: 33,229
 REFERENCE/DOCKET NUMBER: TUV-0855
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1210 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-320-559-26

Query Match 6.0%; Score 136; DB 1; Length 1210;
 Best Local Similarity 20.6%; Pred. No. 0.0072;
 Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

92 AKASHKDKKKPQRS-----QAQSPVSKSTRIQNIIDYLSKVK 135
 553 SOHSESKDPPPKSSSKAPAPAPAPPKSKSCQSPAQEPPOQVGTGKPK-----K 607
 QY 136 KIPSDPESGYTDLOERGNDISPFGDQPFKIP---GKGE-----ATGPD 181
 DB 608 PVKASARAGSRISLOGEREPGLPYGSRDQTSKDKPKVKTKGRPRAASNEPKPAVPSS 667
 QY 182 EKGDIOTGAPSEAS-----THLDTKKPGY-----NEIPRENGANTIGTRDE 227
 DB 668 EKKKHKSSLPAPSKALSGEPKADVEDRTPEHFALVPLTESQGPSSGSRISGCRQA 727
 QY 228 TAKEADAVSVLVEGSDNDIMGSTNFKELPGREGNRV-----DAGSQNAHQKVE 276
 DB 728 VVVCDSRKRDLPLRDTKLISPLRDTPPQSLMVKITLIDLSRIPQPPGKSGRQKAE 787
 QY 277 FHYPPAPSEKREKSSDAESTNNELPKNGKSTRGVDSNRNATLNEKQRFPSK 336
 DB 788 DKOPPAKKSSEKSSSSS-----SKLAKRKGEAERDC-----NKKIR----- 828
 QY 337 KSGQLIPSRGLDNEIKNEMDSFNGPSHENIT-----HGKHYVPHRQNNSTRNK 388
 DB 829 -----LEKTEKSSSSSSSHKESKTKSRPSQSSKEMLPPEPVSSSSQKP 877
 QY 389 GMPQCKGS-----WGRQP-----HNNRRFSSKRRDDSSSSSSSSSS---SDGD 430
 DB 878 AKPALKSRREADTCGQDPKPSASSTKSNHKDSSIPKORAVEGKSSRSSSEHKSSGD 935

RESULT 8
 US-08-545-860D-26
 Sequence 26, Application US/08545860D
 Patent No. 6040140
 GENERAL INFORMATION:
 APPLICANT: Croce, Carlo
 APPLICANT: Canaan, Eli
 TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
 TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
 TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
 ADDRESSER: No. 6040140is
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/545,860D
 FILING DATE: 07-MAR-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04496
 FILING DATE: 22-APR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/10930
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/327,392
 FILING DATE: 19-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/320,559
 FILING DATE: 11-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/062,443
 FILING DATE: 14-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/971,094
 FILING DATE: 30-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/888,839
 FILING DATE: 27-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/805,093
 FILING DATE: 11-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Deluca Esq., Mark
 REGISTRATION NUMBER: 33,229
 REFERENCE/DOCKET NUMBER: TUV-1262
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1210 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-545-860D-26

Query Match 6.0%; Score 136; DB 3; Length 1210;
 Best Local Similarity 20.6%; Pred. No. 0.0072;
 Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

92 AKASHKDKKKPQRS-----QAQSPVSKSTRIQNIIDYLSKVK 135
 553 SOHSESKDPPPKSSSKAPAPAPAPPKSKSCQSPAQEPPOQVGTGKPK-----K 607
 QY 136 KIPSDPESGYTDLOERGNDISPFGDQPFKIP---GKGE-----ATGPD 181
 DB 608 PVKASARAGSRISLOGEREPGLPYGSRDQTSKDKPKVKTKGRPRAASNEPKPAVPSS 667
 QY 182 EKGDIOTGAPSEAS-----THLDTKKPGY-----NEIPRENGANTIGTRDE 227
 DB 668 EKKKHKSSLPAPSKALSGEPKADVEDRTPEHFALVPLTESQGPSSGSRISGCRQA 727
 QY 228 TAKEADAVSVLVEGSDNDIMGSTNFKELPGREGNRV-----DAGSQNAHQKVE 276

DB 728 VVQEDSRKDRPLPLRDTKLLSPRLDTPPQSLMVKITLILSRIPQPGKSGRQKAE 787
CY 277 FHYPPAPSKERKKGSSDAASTYNNEIPKNGKSTKGVDSNRNQTLINEKORFPGK 336
DB 788 DKQPPAGKHSERKSSDS-----SKLAKRKGEAEKDC-----NKLR----- 828
CY 337 KSGGLPIPSRGIDNEIKEMDSFNQPSHENTIT-----HGKTYVPHRONNSTRNK 388
DB 829 -----LEKIKSGSSSSSHKESKTKPRSSQSSKXEMLPPEVSSSQKP 877
CY 389 GMPQKGS-----WGRQ-----HNRKFRSSRRDSSSSSSSSSE---SDGP 430
DB 878 AKPALKRSREADTGQDPPKASSTKSNHKOSSIPKQRYVEGKSSSSSHKSSGD 935

RESULT 9

PCT-US94-04496-26
Sequence 26, Application PC/TUS9404496
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the ALL-1
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca Reg., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1210 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-04496-26

Query Match 6.0%; Score 136; DB 5; Length 1210;
Best Local Similarity 20.6%; Pred. No. 0.0072;
Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;
CY 92 AKAHSDKKKQKQDS-----QAQKSPYKSKSTHICINIDYKHLKSVK 135
DB 553 SEHSSSKPPSPSSSKAPRAPEAPHPGKSCQKSPAQDPPQQTGVTQKPK-----K 607
CY 136 KIPSPDESGYTDLOERDNDISPFSGDQPFKIDP-----GKGE-----ATGPD 181
DB 608 PVKASARASRTSLIGEREPEGLLPYGSRTQSKDKPKVTKGRPALAANEKPAVPPSS 667
CY 182 EKGDIOTGAPGSEAS-----THLDTKKPGY-----NEIPERENGANTIGTDE 227
DB 668 EKKGHKSLPAPKALSGPEPAKDNVEDRTPFHVALVPLTESQGPSPHSGSGSRTSGCROA 727

CY 228 TAKEADAVDVSLVSGSNDINGSTNFKELPGSEGNRV-----DAGQNAHQKTE 276
DB 728 VVQEDSRKDRPLPLRDTKLLSPRLDTPPQSLMVKITLILSRIPQPGKSGRQKAE 787
CY 277 FHYPPAPSKERKKGSSDAASTYNNEIPKNGKSTKGVDSNRNQTLINEKORFPGK 336
DB 788 DKQPPAGKHSERKSSDS-----SKLAKRKGEAEKDC-----NKLR----- 828
CY 337 KSGGLPIPSRGIDNEIKEMDSFNQPSHENTIT-----HGKTYVPHRONNSTRNK 388
DB 829 -----LEKIKSGSSSSSHKESKTKPRSSQSSKXEMLPPEVSSSQKP 877
CY 389 GMPQKGS-----WGRQ-----HNRKFRSSRRDSSSSSSSSSE---SDGP 430
DB 878 AKPALKRSREADTGQDPPKASSTKSNHKOSSIPKQRYVEGKSSSSSHKSSGD 935

RESULT 10

US-07-814-964-11
Sequence 11, Application US/07814964
Patent No. 5359047
GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pil, Peter M.
APPLICANT: Brown, Steven
APPLICANT: Kelleet, Patti
APPLICANT: Essigmann, John M.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,964
FILING DATE: 19911226
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787A2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 11
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Drosophila melanogaster
IMMEDIATE SOURCE:
CLONE: Drosophila ssRP (predicted)
FEATURE:
NAME/KEY: Domain
LOCATION: 458..507

MEDIUM TYPE: Floppy disk

D5 614 -----HDEMRNYKPEAGGDS DNEKG---GNSSKKKKI 612

QY 400 QPHSNR-----FSSRR--RDDSSESDSGSSSE-----SDGD 430
Db 643 EPSPKKANTSGSGFKSKEYISDDSTSSDDEKNEPAKKSKPPSPD 691

RESULT 12
US-08-328-809-6
Sequence 6, Application US/08328809
Patent No. 5705334

GENERAL INFORMATION:
APPLICANT: Lippard, Stephen J.
APPLICANT: Essigmann, John M.
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pili, Plecter M.
APPLICANT: Brown, Steven
APPLICANT: Kellelt, Patti
TITLE OF INVENTION: Uses For DNA Structure-Specific
TITLE OF INVENTION: Recognition Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Patent Administrator, Testa, Hurwitz & Thibault
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328, 809
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fenton, Gillian M.
REGISTRATION NUMBER: 36, 508
REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
ORIGINAL SOURCE:

ORGANISM: Drosophila melanogaster
IMMEDIATE SOURCE:

CLONE: Drosophila SSRP (predicted)
FEATURE:

NAME/KEY: Domain
LOCATION: 458..507
OTHER INFORMATION: /label= Acidic

FEATURE:
NAME/KEY: Domain
LOCATION: 518..547
OTHER INFORMATION: /label= Basic I

FEATURE:
NAME/KEY: Domain
LOCATION: 547..620
OTHER INFORMATION: /label= HMG

FEATURE:
NAME/KEY: Domain
LOCATION: 632..649
OTHER INFORMATION: /label= Basic II

FEATURE:
NAME/KEY: Domain
LOCATION: 649..723
OTHER INFORMATION: /label= Basic III

FEATURE:
NAME/KEY: Domain
LOCATION: 723..809
OTHER INFORMATION: /label= Basic IV

FEATURE:
NAME/KEY: Domain
LOCATION: 809..885
OTHER INFORMATION: /label= Basic V

FEATURE:
NAME/KEY: Domain
LOCATION: 885..961
OTHER INFORMATION: /label= Basic VI

FEATURE:
NAME/KEY: Domain
LOCATION: 961..1037
OTHER INFORMATION: /label= Basic VII

FEATURE:
NAME/KEY: Domain
LOCATION: 1037..1113
OTHER INFORMATION: /label= Basic VIII

FEATURE:
NAME/KEY: Domain
LOCATION: 1113..1189
OTHER INFORMATION: /label= Basic IX

FEATURE:
NAME/KEY: Domain
LOCATION: 1189..1265
OTHER INFORMATION: /label= Basic X

LOCATION: 657..723
OTHER INFORMATION: /label= Mixed Charge
US-08-328-809-6

Query Match 5.9%; Score 135.5; DB 1; Length 723;
Best Local Similarity 23.2%; Pred. No. 0.0038;
Matches 81; Conservative 37; Mismatches 114; Indels 117; Gaps 18;

QY 126 DYLR---HLSKVKIPEDFGSGYTDQEGNDISFSGDGPFPDIPG-KGEATPD 180
Db 416 DYTQKKLHVNMGR---DKSGYDV-DFGSD---NENEDAVLAKKAPRKE 464
QY 181 LEGKDIOGTFAGPSEASTHLDTKKPGYNEIPERENGNTIGTRDETAKADAVVSLV 240
Db 465 EDDDD---GDSESTDEDF-KPNENESDAVEYVSNEVSDSD---DSDASG--- 510
QY 241 EGSNDIWSYTFKELPGREGNRVDAGSONAQKVEFYHYPAPKEKEKES 292
Db 511 -GGGSDGAKKK 562
QY 293 ---SDAAS---TNYNEIPNGKSTRKGVDSNRQATLINEKOPPSKSGQL 341
Db 563 MMTNDTRESIKRNPGLKTEIAKGGEMMKELDKSKWDAKAKQRY----- 613
QY 342 PTPSRGLDNEIKNENDSRGSHENITRGRKHYVPRQNNSTRNKGMPGKSGWR 399
Db 614 -----HDEMRNYKPPAGSDSDNEKG---GSKSKKKT 642

RESULT 13
US-08-866-840-6
Sequence 6, Application US/08866840
Patent No. 6475791

GENERAL INFORMATION:
APPLICANT: Lippard, Stephen J.
APPLICANT: Essigmann, John M.
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pili, Plecter M.
APPLICANT: Brown, Steven
APPLICANT: Kellelt, Patti
TITLE OF INVENTION: Uses For DNA Structure-Specific
TITLE OF INVENTION: Recognition Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Patent Administrator, Testa, Hurwitz & Thibault
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866, 840
FILING DATE: 02-JUN-1997

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fenton, Gillian M.
REGISTRATION NUMBER: 36, 508
REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
ORIGINAL SOURCE:

ORGANISM: Drosophila melanogaster
IMMEDIATE SOURCE:

CLONE: Drosophila SSRP (predicted)
FEATURE:

NAME/KEY: Domain
LOCATION: 458..507
OTHER INFORMATION: /label= Acidic

FEATURE:
NAME/KEY: Domain
LOCATION: 518..547
OTHER INFORMATION: /label= Basic I

FEATURE:
NAME/KEY: Domain
LOCATION: 547..620
OTHER INFORMATION: /label= HMG

FEATURE:
NAME/KEY: Domain
LOCATION: 632..649
OTHER INFORMATION: /label= Basic II

TITLE OF INVENTION: Protein and Uses Therefor
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: 2 Millitia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/11107
 FILING DATE: 19921218
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/539,906
 FILING DATE: 18-JUN-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: MIT-4787AAA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 723 amino acids

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? TYPE: AMINO ACID
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? ORIGINAL SOURCE:
? ORGANISM: Drosophila melanogaster
? IMMEDIATE SOURCE:
? CLONE: Drosophila SSRP (predicted)
? FEATURE:
? NAME/KEY: Domain
? LOCATION: 458..507
? OTHER INFORMATION: /label= Acidic
? FEATURE:
? NAME/KEY: Domain
? LOCATION: 518..547
? OTHER INFORMATION: /label= Basic I
? FEATURE:
? NAME/KEY: Domain
? LOCATION: 547..620
? OTHER INFORMATION: /label= HMG-box
? FEATURE:
? NAME/KEY: Domain
? LOCATION: 632..649
? OTHER INFORMATION: /label= Basic II
? FEATURE:
? NAME/KEY: Domain
? LOCATION: 657..723
? OTHER INFORMATION: /label= Mixed Charge
PCT-US92-1107-11

Query Match          5.9%; Score 135.5; DB 5; Length 723;
Best Local Similarity 23.2%; Pred.No.0.0038;
Matches      81; Conservative   37; Mismatches 114; Indels 117; Gaps    18

QY      126 DYLK-----HLSKVKKIPSPDFSGSYGTDLQERGDNDISPFSGDGPFPKDI PG-KGEATGPD 180
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
DB      416 DYITTKKLIVSNWGR----DKSGKYDV-DFGDSP-----NENEPDAYIAARKAKAREKE 464
QY      181 LEGKDIGTGFAPSPAESTHLDTFKPGYNEI PEREENGANTGTGTRDETAKEDAVDSILV 240
Db      465 EDDDD-----GDSDESTDED F-KPENESDPVAEEYSNVASDSD-- -DSDAG----- 510
QY      241 EGSDINMSGTNFKELPGREGNRVADAGSNAHQGKTFFHYPPARPSRKRREKS----- 292
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Result No.	Score	Query	Length	DB	ID	Description
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2	2276	99.9	525	10	US-09-794-422-6	Sequence 6, Appl
3	2276	99.9	525	14	US-10-111-840-1	Sequence 1, Appl
4	2276	99.9	540	10	US-09-794-422-46	Sequence 46, Appl
5	2276	99.9	556	10	US-09-794-422-8	Sequence 8, Appl
6	2269	99.6	525	9	US-09-814-550-8	Sequence 2, Appl
7	983.5	43.2	441	10	US-09-794-422-2	Sequence 4, Appl
8	938.5	41.2	435	10	US-09-794-422-2	Sequence 2, Appl
9	514	22.6	97	9	US-09-812-485A-1	Sequence 1, Appl
10	246	10.8	47	9	US-09-812-485A-2	Sequence 2, Appl
11	235	10.3	47	9	US-09-812-485A-3	Sequence 3, Appl
12	225	10.0	47	9	US-09-812-485A-4	Sequence 4, Appl
13	218	9.6	40	9	US-09-812-485A-23	Sequence 23, Appl
14	216	9.5	44	9	US-09-812-485A-5	Sequence 6, Appl
15	215	9.4	44	9	US-09-812-485A-5	Sequence 5, Appl

16	214.5	9.4	45	9	US-09-812-4858-27	Sequence 27, Appl
17	198.5	8.7	41	9	US-09-812-4858-8	Sequence 8, Appl
18	190.5	8.4	40	9	US-09-812-4858-24	Sequence 24, Appl
19	188.5	8.3	40	9	US-09-812-4858-32	Sequence 32, Appl
20	182	8.0	37	9	US-09-812-4858-7	Sequence 7, Appl
21	180	7.9	38	9	US-09-812-4858-10	Sequence 10, Appl
22	163.5	7.2	35	9	US-09-812-4858-25	Sequence 25, Appl
23	157.5	6.9	35	9	US-09-812-4858-28	Sequence 28, Appl
24	153.5	6.7	33	9	US-09-812-4858-30	Sequence 30, Appl
25	152	6.7	1253	14	US-10-363-799-2	Sequence 2, Appl
26	150	6.6	32	9	US-09-812-4858-12	Sequence 12, Appl
27	148	6.5	1591	12	US-10-210-172-66	Sequence 66, Appl
28	148	6.5	1884	9	US-09-785-7704-17	Sequence 17, Appl
29	148	6.5	1907	9	US-09-785-7704-16	Sequence 16, Appl
30	148	6.5	1907	12	US-10-210-172-64	Sequence 64, Appl
31	146.5	6.4	33	9	US-09-812-4858-31	Sequence 31, Appl
32	145	6.4	2174	14	US-10-087-887-87	Sequence 87, Appl
33	145	6.4	940	15	US-10-108-260A-3781	Sequence 3781, Ap
34	144.5	6.3	665	10	US-09-820-848A-107	Sequence 107, App
35	144.5	6.3	31	9	US-09-812-4858-33	Sequence 33, Appl
36	142.5	6.1	31	9	US-09-812-4858-36	Sequence 36, Appl
37	140	6.1	772	14	US-10-153-668-302	Sequence 302, App
38	137.5	6.0	30	9	US-09-812-4858-26	Sequence 26, Appl
39	136	6.0	1210	14	US-10-205-8823-264	Sequence 264, App
40	135	5.9	1742	12	US-10-215-383-4	Sequence 4, Appl
41	134.5	5.9	1115	13	US-10-153-273-17	Sequence 2, Appl
42	133.5	5.9	1462	14	US-10-287-218-12	Sequence 17, Appl
43	133	5.8	748	15	US-10-108-260A-3747	Sequence 3747, Ap
44	133	5.8	1069	12	US-10-424-599-25931	Sequence 25931, A
45	132	5.8	1633	12	US-10-282-122A-70437	Sequence 70437, A

ALIGNMENTS

RESULT 1

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US-09-794-422-34
: Sequence 44, Application US/09794422
: Publication No. US20030166239A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Brown, Thomas A.
: APPLICANT: De Wet, Jeffrey R.
: APPLICANT: Gowen, Lori C.
: APPLICANT: Hames, Lynn M.
: TITLE OF INVENTION: Mammalian Osteoregulin
: FILE REFERENCE: PC10445
: CURRENT APPLICATION NUMBER: US/09/794,422
: CURRENT FILING DATE: 2001-02-27
: PRIOR APPLICATION NUMBER: 60/185,617
: PRIOR FILING DATE: 2000-02-29
: PRIOR APPLICATION NUMBER: 60/234,500
: PRIOR FILING DATE: 2000-09-22
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO. 34
:
: LENGTH: 509
:
: TYPE: prt
:
: ORGANISM: Homo sapiens
:
: US-09-794-422-34

```

Query Match	99.9%;	Score 2276;	DB 10;	Length 509;
Best Local Similarity	99.8%;	Pred. No. 7,6e-173;		
Matches 429;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	VNKEYSISNKEENHNGLJMSITPKSTGNKGPPDDGDAISKLDHEEYGAALIRNNQHM	60	
	:			
Db	80	LNKEYSISNKEENHNGLJMSITPKSTGNKGPPDDGDAISKLDHEEYGAALIRNNQHM	139	
QY	61	GPVTAIKLIGENKENTPRNVLTIIIPASNTYAKAHSKDKKPPQDSQAQSFPVSKSTHR	120	
Db	140	GPVTAIKLIGENKENTPRNVLTIIIPASNTYAKAHSKDKKPPQDSQAQSFPVSKSTHR	199	
QY	121	IQHIDVLKHLKSLVKKIPDPDFGSGVTDLDQEGDNDIPFGDQGFPMIDPGKEATGPD	180	

Db 200 IQHNIDYKHLKSVKXKIPSDFEQGYTDLQERDNDISPFSGDQGFKDIPOKGEATGPD 259
Qy 181 LEGKDIQTGFPAGPSEASTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 240
Db 260 LEGKDIQTGFPAGPSEASTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 319
Qy 241 EGSNDIMGSTNFKELPQREGNRVDAQSNQAHQGVKVEFHYPPAPSKKKEGSSDAEESTN 300
Db 320 EGSNDIMGSTNFKELPQREGNRVDAQSNQAHQGVKVEFHYPPAPSKKKEGSSDAEESTN 379
Qy 301 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 360
Db 380 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 439
Qy 361 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRDDSSSD 420
Db 440 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRDDSSSD 499
Qy 421 SGSSSESDDG 430
Db 500 SGSSSESDDG 509

RESULT 2

US-09-794-422-6

; Sequence 6, Application US/09794422

; Publication No. US20030166239A1

; GENERAL INFORMATION:

; APPLICANT: Brown, Thomas A.

; APPLICANT: De Wet, Jeffrey R.

; APPLICANT: Gowen, Lori C.

; APPLICANT: Hames, Lynn M.

; TITLE OF INVENTION: Mammalian Osteoregulins

; FILE REFERENCE: PCI0445

; CURRENT APPLICATION NUMBER: US/09/794,422

; CURRENT FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: 60/185,617

; PRIOR FILING DATE: 2000-02-29

; PRIOR APPLICATION NUMBER: 60/234,500

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 525

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-794-422-6

Query Match 99.9%; Score 2276; DB 10; Length 525;
Best Local Similarity 99.8%; Pred. No. 88-173; 0; Indels 0; Gaps 0;
Matches 429; Conservative 1; Mismatches 0;

Qy 1 VNKEYSISNKENTHGLRMSIYPKSTGNKGFEDGDDAISKLHDQBEYGAALIRNNQHM 60
Db 96 LNKEYSISNKENTHGLRMSIYPKSTGNKGFEDGDDAISKLHDQBEYGAALIRNNQHM 155
Qy 61 GPVTAIKLGEENKENTPRVNLNIPASMYAKAHSKDKKKPQDSQAKSPVKSKSTHR 120
Db 156 GPVTAIKLGEENKENTPRVNLNIPASMYAKAHSKDKKKPQDSQAKSPVKSKSTHR 215
Qy 121 IQHNIDYKHLKSVKXKIPSDFEQGYTDLQERDNDISPFSGDQGFKDIPOKGEATGPD 180
Db 216 IQHNIDYKHLKSVKXKIPSDFEQGYTDLQERDNDISPFSGDQGFKDIPOKGEATGPD 275
Qy 181 LEGKDIQTGFPAGPSEASTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 240
Db 276 LEGKDIQTGFPAGPSEASTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 335
Qy 241 EGSNDIMGSTNFKELPQREGNRVDAQSNQAHQGVKVEFHYPPAPSKKKEGSSDAEESTN 300
Db 336 EGSNDIMGSTNFKELPQREGNRVDAQSNQAHQGVKVEFHYPPAPSKKKEGSSDAEESTN 395

Qy 301 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 360
Db 396 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 455
Qy 361 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRDDSSSD 420
Db 456 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRDDSSSD 515
Qy 421 SGSSSESDDG 430
Db 516 SGSSSESDDG 525

RESULT 3

US-10-311-840-1

; Sequence 1, Application US/10311840

; Publication No. US20030175808A1

; GENERAL INFORMATION:

; APPLICANT: KUROKAWA, Tomofumi

; APPLICANT: YAMADA, Takao

; APPLICANT: MORIMOTO, Shigeto

; TITLE OF INVENTION: No. US20030175808A1el Protein and its DNA

; FILE REFERENCE: 2738USOP

; CURRENT APPLICATION NUMBER: US/10/311,840

; CURRENT FILING DATE: 2002-12-18

; PRIOR APPLICATION NUMBER: PCT/JP01/05263

; PRIOR FILING DATE: 2001-06-20

; PRIOR APPLICATION NUMBER: JP 2000-191088

; PRIOR FILING DATE: 2000-06-21

; NUMBER OF SEQ ID NOS: 10

; SEQ ID NO 1

; LENGTH: 525

; TYPE: PRT

; ORGANISM: Human

US-10-311-840-1

Query Match 99.9%; Score 2276; DB 14; Length 525;
Best Local Similarity 99.8%; Pred. No. 88-173; 0; Indels 0; Gaps 0;
Matches 429; Conservative 1; Mismatches 0;

Qy 1 VNKEYSISNKENTHGLRMSIYPKSTGNKGFEDGDDAISKLHDQBEYGAALIRNNQHM 60
Db 96 LNKEYSISNKENTHGLRMSIYPKSTGNKGFEDGDDAISKLHDQBEYGAALIRNNQHM 155
Qy 61 GPVTAIKLGEENKENTPRVNLNIPASMYAKAHSKDKKKPQDSQAKSPVKSKSTHR 120
Db 156 GPVTAIKLGEENKENTPRVNLNIPASMYAKAHSKDKKKPQDSQAKSPVKSKSTHR 215
Qy 121 IQHNIDYKHLKSVKXKIPSDFEQGYTDLQERDNDISPFSGDQGFKDIPOKGEATGPD 180
Db 216 IQHNIDYKHLKSVKXKIPSDFEQGYTDLQERDNDISPFSGDQGFKDIPOKGEATGPD 275
Qy 181 LEGKDIQTGFPAGPSEASTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 240
Db 276 LEGKDIQTGFPAGPSEASTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 335
Qy 241 EGSNDIMGSTNFKELPQREGNRVDAQSNQAHQGVKVEFHYPPAPSKKKEGSSDAEESTN 300
Db 336 EGSNDIMGSTNFKELPQREGNRVDAQSNQAHQGVKVEFHYPPAPSKKKEGSSDAEESTN 395
Qy 301 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 360
Db 396 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 455
Qy 361 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRDDSSSD 420
Db 456 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRDDSSSD 515
Qy 421 SGSSSESDDG 430
Db 516 SGSSSESDDG 525

```
RESULT 4
US-09-794-422-46
; Sequence 46, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 46
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-46

Query Match          99.9%; Score 2276; DB 10; Length 540;
Best Local Similarity 99.8%; Pred. No. 8.3e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VNKEYSISNKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDQEYGAALIRNNQHIM 60
Db      111 LNKEYSISNKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDQEYGAALIRNNQHIM 170
QY      61 GPTAIKLLGEENKENTPRNVLNIIIPASMYAKAHSKDKKKPQRSQAOKSPVKSKSTHR 120
Db      171 GPTAIKLLGEENKENTPRNVLNIIIPASMYAKAHSKDKKKPQRSQAOKSPVKSKSTHR 230
QY      121 IQHNIDYLKHLKSVKVKIIPSDFEFGSGYTDLQERGDNDISPFSGDGOPFKDIPKGGEATGPD 180
Db      231 IQHNIDYLKHLKSVKVKIIPSDFEFGSGYTDLQERGDNDISPFSGDGOPFKDIPKGGEATGPD 290
QY      181 LEGKDIQTGFAGPSEAEATHLDTKPKGYNEIIPEREENGNTIGTRDETAKEADAVDVSLV 240
Db      291 LEGKDIQTGFAGPSEAEATHLDTKPKGYNEIIPEREENGNTIGTRDETAKEADAVDVSLV 350
QY      241 EGSNDIMGSTNFKELPGRGNRVDAQSQNAHOGKVEFHYPPAPSKKEKKGSSDAEAESTN 300
Db      351 EGSNDIMGSTNFKELPGRGNRVDAQSQNAHOGKVEFHYPPAPSKKEKKGSSDAEAESTN 410
QY      301 YNEIPKNGKSTRKGVDSHNRNQATLNEKQRPFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 360
Db      411 YNEIPKNGKSTRKGVDSHNRNQATLNEKQRPFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 470
QY      361 GPSHENIITHGRKYHVPHRQNNSTRNKMGPOKGSWGRQPHSNRRFSSRRDDSSSED 420
Db      471 GPSHENIITHGRKYHVPHRQNNSTRNKMGPOKGSWGRQPHSNRRFSSRRDDSSSED 530
QY      421 SGSSSESDDG 430
Db      531 SGSSSESDDG 540

RESULT 5
US-09-794-422-8
; Sequence 8, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
```

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US-09-794-422-8
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 8
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-8

Query Match          99.9%; Score 2276; DB 10; Length 556;
Best Local Similarity 99.8%; Pred. No. 8.6e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VNKEYSISNKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDQEYGAALIRNNQHIM 60
Db      127 LNKEYSISNKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDQEYGAALIRNNQHIM 186
QY      61 GPTAIKLLGEENKENTPRNVLNIIIPASMYAKAHSKDKKKPQRSQAOKSPVKSKSTHR 120
Db      187 GPTAIKLLGEENKENTPRNVLNIIIPASMYAKAHSKDKKKPQRSQAOKSPVKSKSTHR 246
QY      121 IQHNIDYLKHLKSVKVKIIPSDFEFGSGYTDLQERGDNDISPFSGDGOPFKDIPKGGEATGPD 180
Db      247 IQHNIDYLKHLKSVKVKIIPSDFEFGSGYTDLQERGDNDISPFSGDGOPFKDIPKGGEATGPD 306
QY      181 LEGKDIQTGFAGPSEAEATHLDTKPKGYNEIIPEREENGNTIGTRDETAKEADAVDVSLV 240
Db      307 LEGKDIQTGFAGPSEAEATHLDTKPKGYNEIIPEREENGNTIGTRDETAKEADAVDVSLV 366
QY      241 EGSNDIMGSTNFKELPGRGNRVDAQSQNAHOGKVEFHYPPAPSKKEKKGSSDAEAESTN 300
Db      367 EGSNDIMGSTNFKELPGRGNRVDAQSQNAHOGKVEFHYPPAPSKKEKKGSSDAEAESTN 426
QY      301 YNEIPKNGKSTRKGVDSHNRNQATLNEKQRPFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 360
Db      427 YNEIPKNGKSTRKGVDSHNRNQATLNEKQRPFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 486
QY      361 GPSHENIITHGRKYHVPHRQNNSTRNKMGPOKGSWGRQPHSNRRFSSRRDDSSSED 420
Db      487 GPSHENIITHGRKYHVPHRQNNSTRNKMGPOKGSWGRQPHSNRRFSSRRDDSSSED 546
QY      421 SGSSSESDDG 430
Db      547 SGSSSESDDG 556

RESULT 6
US-09-814-550-2
; Sequence 2, Application US/09814550
; Patent No. US20020102641A1
; GENERAL INFORMATION:
; APPLICANT: Schiavi, Susan
; APPLICANT: Madden, Stephen
; APPLICANT: Manavalan, Parthasarathy
; APPLICANT: Levine, Michael
; APPLICANT: Jan de Beur, Suzanne
; TITLE OF INVENTION: ONCOGENIC OSTEOBLAST-RELATED GENE 1
; FILE REFERENCE: 5014US
; CURRENT APPLICATION NUMBER: US/09/814,550
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,786
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/241,598
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 525
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Db 206 V-----SGSSNVEIVDPHTNGLSSNEIPQRECHIGGAYATRGKTAQGAGSADVSILVEGSNE 261
Qy 246 IMGSTNFXELPQREGRNRYDAGSQNAHQKVEFFHYPPAPSKKREKGGSDAAESTNYNEIP 305
Db 262 ITGSKFRELPGKGRNRYDAGSQNAHQKVEFFHYPPAPSKKREKGGSDAAESTNYNEIP 321
Qy 306 KNGKSTKGVVDHNRNQTALNEKQRPSPKSKQGLPIPSRGLDNEIKNEMWDSFNGPSHE 365
Db 322 KSSKGGASKDAESKGNQVTLTESQRFPGKGGQS-----SHSLGNEVKSEEDSSNSLSRE 377
Qy 366 NI-ITHGRKYHVPHRQNNSTRNKGMPQKGSW-GRQPHSNRRSSRRRDDSSSSSSGS 423
Db 378 GIATHRATSH-----PTNRGMSQRRGSWASRRPHRRVSTRQR-DSSSSSSSGS 428
Qy 424 SSESQGD 430
Db 429 SSESQGD 435

RESULT 9
US-09-812-485A-1
; Sequence 1, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-1

Query Match 22.6%; Score 514; DB 9; Length 97;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 105 DSOAQSPVKSKSTHRIQHNIDYLKHLKSVKVKIPSPDFEGSGYTDLQERGDNDISPFSGDG 164
Db 1 DSOAQSPVKSKSTHRIQHNIDYLKHLKSVKVKIPSPDFEGSGYTDLQERGDNDISPFSGDG 60

Qy 165 QPPKIDIPGKGATGPDLGKDIQTGFPAGPSEASTHL 201
Db 61 QPPKIDIPGKGATGPDLGKDIQTGFPAGPSEASTHL 97

RESULT 10
US-09-812-485A-2
; Sequence 2, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-2

Query Match 10.8%; Score 246; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 AQSPVKSKSTHRIQHNIDYLKHLKSVKVKIPSPDFEGSGYTDLQERGD 154
Db 1 AQSPVKSKSTHRIQHNIDYLKHLKSVKVKIPSPDFEGSGYTDLQERGD 47

RESULT 11
US-09-812-485A-4
; Sequence 4, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-4

Query Match 10.3%; Score 235.5; DB 9; Length 47;
Best Local Similarity 94.0%; Pred. No. 1.2e-11;
Matches 47; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 105 DSOAQSPVKSKSTHRIQHNIDYLKHLKSVKVKIPSPDFEGSGYTDLQERGD 154
Db 1 DSOAQSPVKSKSTHRIQHNIDYLKHLKSVKVKIPSPDFEGSGYTD---RGD 47

RESULT 12
US-09-812-485A-3
; Sequence 3, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: peptidic compound
US-09-812-485A-3

FEATURE:
OTHER INFORMATION: peptidic compound
US-09-812-485A-3

Query Match 10.0%; Score 229; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.9e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 108 AQSAPVSKSTHRIQHNIDYKHLKSKVKIPSPDFEGSGYTDLQER 151
Db 4 AQSAPVSKSTHRIQHNIDYKHLKSKVKIPSPDFEGSGYTDLQER 47

RESULT 13

US-09-812-485A-23
Sequence 23, Application US/09912485A
Publication No. US20020197267A1
GENERAL INFORMATION:
APPLICANT: Kumagai, Yoshinari
APPLICANT: Blacher, Russel
APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
CURRENT FILING DATE: 2001-03-19
PRIOR FILING DATE: 09/641,034
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptidic compound
US-09-812-485A-23

Query Match 9.6%; Score 218; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 152 RGNNDISPPSGDQPKDIPGKGATGPDLEGKDITGFA 191
Db 1 RGNNDISPPSGDQPKDIPGKGATGPDLEGKDITGFA 40

RESULT 14

US-09-812-485A-6
Sequence 6, Application US/09812485A
Publication No. US20020197267A1
GENERAL INFORMATION:
APPLICANT: Kumagai, Yoshinari
APPLICANT: Blacher, Russel
APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
CURRENT FILING DATE: 2001-03-19
PRIOR FILING DATE: 09/641,034
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 44
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptidic compound
US-09-812-485A-6

Query Match 9.5%; Score 216; DB 9; Length 44;

Best Local Similarity 88.0%; Pred. No. 3.8e-10;
Matches 44; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
QY 105 DSQAQSPVSKSTHRIQHNIDYKHLKSKVKIPSPDFEGSGYTDLQERGD 154
Db 1 DSQAQSPVSKSTHRIQHNIDYKHLKSKVKIPSPDFEGSG-----RGD 44

RESULT 15

US-09-812-485A-5
Sequence 5, Application US/09812485A
Publication No. US20020197267A1
GENERAL INFORMATION:
APPLICANT: Kumagai, Yoshinari
APPLICANT: Blacher, Russel
APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
CURRENT FILING DATE: 2001-03-19
PRIOR FILING DATE: 09/641,034
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 44
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: peptidic compound
US-09-812-485A-5

Query Match 9.4%; Score 215; DB 9; Length 44;
Best Local Similarity 100.0%; Pred. No. 4.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 111 SPVSKSTHRIQHNIDYKHLKSKVKIPSPDFEGSGYTDLQER 151
Db 4 SPVSKSTHRIQHNIDYKHLKSKVKIPSPDFEGSGYTDLQER 44

Search completed: March 24, 2004, 21:37:35
Job time : 47 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 29, 2004, 01:29:51 ; Search time 125 Seconds
(without alignments)
1909.031 Million cell updates/sec

Title: US-09-700-696C-2
Perfect score: 2279
Sequence: 1 VNKEYSINKENTHNGLRMS.....RRDSSSSSSGSSSSSDGD 430

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 100%
Listing first 45 summaries

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -p2n.model -DEV-xlh

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-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09700696 @CGN 1 1.56 @runat_24032004_151402_1151 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT_DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A-COMB.seq:
2: /cgn2_6/ptodata/2/ina/5B-COMB.seq:
3: /cgn2_6/ptodata/2/ina/6A-COMB.seq:
4: /cgn2_6/ptodata/2/ina/6B-COMB.seq:
5: /cgn2_6/ptodata/2/ina/PCTUS-COMB.seq:
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2279	100.0	1655	US-10-132-920B-1	Sequence 1, Appli
2	2276	99.9	2013	US-10-132-920B-26	Sequence 26, Appli
3	150	6.6	6755	US-08-931-999-4	Sequence 4, Appli
4	140	6.1	2690	US-08-524-757-11	Sequence 11, Appli
5	138.5	6.1	2384	US-07-814-964-10	Sequence 10, Appli
6	138.5	6.1	2384	US-08-258-443-10	Sequence 10, Appli
7	138.5	6.1	2384	US-08-328-809-5	Sequence 5, Appli
8	138.5	6.1	2384	US-08-866-840-5	Sequence 5, Appli
9	138.5	6.1	2384	PCT-US92-11107-10	Sequence 10, Appli
10	137	6.0	9370	US-08-320-559-27	Sequence 27, Appli
11	137	6.0	9370	US-08-545-860D-3	Sequence 27, Appli
12	137	6.0	9370	PCT-US94-04496-27	Sequence 27, Appli

13	137	6.0	9391	1	US-08-320-559-25	Sequence 25, Appli
14	137	6.0	9391	3	US-08-545-860D-25	Sequence 25, Appli
15	137	6.0	9391	5	PCT-US94-04496-25	Sequence 25, Appli
16	135	5.9	5406	4	US-09-386-962C-1	Sequence 1, Appli
17	134.5	5.9	4084	2	US-08-568-459A-1	Sequence 1, Appli
18	134.5	5.9	4084	2	US-08-487-826B-1	Sequence 1, Appli
19	134.5	5.9	4084	4	US-09-210-288-1	Sequence 1, Appli
20	134.5	5.9	4084	6	5198347-5	Patent No. 5198347
21	129	5.7	2712	4	US-09-976-594-374	Patent No. 5198347
22	129	5.7	3157	6	5198347-3	Patent No. 5198347
23	127.5	5.6	3707	1	US-08-118-101A-1	Sequence 1, Appli
24	127	5.6	2695	4	US-09-706-197-3	Sequence 3, Appli
25	126.5	5.6	4215	4	US-09-620-312D-295	Sequence 295, Appli
26	126.5	5.6	1393	5	PCT-US93-07261-12	Sequence 12, Appli
27	126.5	5.6	3773	3	US-09-130-242-1	Sequence 1, Appli
28	125.5	5.5	3825	3	US-09-208-742-3	Sequence 3, Appli
29	125.5	5.5	5173	4	US-08-801-308-2	Sequence 2, Appli
30	124.5	5.5	3552	4	US-09-134-001C-693	Sequence 693, Appli
31	123	5.4	1503	3	US-08-999-774A-11	Sequence 11, Appli
32	123	5.4	3534	4	US-09-134-001C-2269	Sequence 2269, Appli
33	123	5.4	4766	5	PCT-US93-07261-10	Sequence 10, Appli
34	123	5.4	6775	4	US-09-620-312D-289	Sequence 289, Appli
35	122.5	5.4	3347	4	US-09-702-705-318	Sequence 318, Appli
36	122.5	5.4	3347	4	US-09-736-457-318	Sequence 318, Appli
37	122.5	5.4	3347	4	US-09-614-124B-318	Sequence 318, Appli
38	122.5	5.4	3347	4	US-09-671-325-318	Sequence 318, Appli
39	122.5	5.4	3347	4	US-09-589-184-318	Sequence 318, Appli
40	122	5.4	2073	4	US-09-134-001C-1731	Sequence 1731, Appli
41	122	5.4	43280	2	US-08-804-227C-1	Sequence 1, Appli
42	121	5.3	2004	1	US-08-471-033-18	Sequence 18, Appli
43	121	5.3	2004	2	US-08-471-044-18	Sequence 18, Appli
44	121	5.3	2004	2	US-08-463-483A-18	Sequence 18, Appli
45	121	5.3	2004	2	US-08-471-046A-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-10-132-920B-1
Sequence 1, Application US/10132920B

Patent No. 6673900
GENERAL INFORMATION:
APPLICANT: Rowe, Peter
TITLE OF INVENTION: A Polypeptide Hormone-Phosphatonin
FILE REFERENCE: BEAR-005CON
CURRENT APPLICATION NUMBER: US/10/132,920B
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 09/434,185
PRIOR FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1655
TYPE: DNA
ORGANISM: Homo sapien
US-10-132-920B-1

Alignment Scores:
Pred. No.: 6.2e-213
Score: 2279.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Length: 1655
Matches: 430
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-700-696C-2 (1-430) x US-10-132-920B-1 (1-1655)

QY 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20

DB 1 GTGAATTAAGAAATATAGTATCATCAACAAAGAAATCACTCAATGCGCTGAGGATGCA 60

QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40


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1  RESULT 3
2  US-08-931-999-4
3  ; Sequence 4, Application US/08931999
4  ; Patent No. 6043219
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Iandolo, John J.
7  ; APPLICANT: Crupper, Scott S.
8  ; TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide
9  ; NUMBER OF SEQUENCES: 4
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: Hovey, Williams, Timmons & Collins
12 ; STREET: 2405 Grand Boulevard, Suite 400
13 ; CITY: Kansas City
14 ; STATE: Missouri
15 ; COUNTRY: U.S.A.
16 ; ZIP: 64108
17 ; COMPUTER READABLE FORM:
18 ; MEDIUM TYPE: Floppy disk
19 ; COMPUTER: IBM PC compatible

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US-09-700-696C-2 (1-430) X US-08-931-999-4 (1-6755)

COMPUTER: IBM PC compatible

Db 767 ----- 767
QY 83 AsnIlelleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysLysPro 102
Db 768 ----- 768
QY 103 GlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArgIleGln 122
Db 798 GATGCCAAGAGTGTAGAGAGCGCTCTGTGTGTAGAGAGAGAAATCACAC----- 848
QY 123 HisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysLysIleProSerAspPheGlu 142
Db 849 ----- 849
QY 143 GlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGly 162
Db 864 ----- 864
QY 163 AspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
Db 891 GACATGCAAGGAGAAACCG---CCCTCTAGTGGCTAAAGAAAGAGAGAGAGAGAG 947
QY 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSer---ThrHisLeu 201
Db 948 GCGACGAGCTGAAGACAGAGAGTGTTCCTCCTCAGAGGCGCTTCAGACCAACACCTG 1007
QY 202 AspThrLysProGlyTyrAsnGluLeuProGluArgGluGluAsnGlyGlyAsnThr 221
Db 1008 ----- 1008
QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuValGlu 241
Db 1044 ----- 1044
QY 242 GlySerAsnAspIleMet-----GlySerThrAsnPheLysGluLeu 255
Db 1089 GGAGCAGGAGACCTTGTCCCAAGGTAAAGAGAGAGGTCTTAAACACTTAAAGACCTCA 1148
QY 256 ProGlyArgGluGlyAsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyVal 275
Db 1149 GAAGGAAAGTCAAAACTTAATTTGTGTAGTAGAAGTCACTGGGTCC---CTCCCTAAAGTT 1205
QY 276 ----- 280
Db 1206 GAGGAGACATATGAGGATGAATTCGAGACCAACCATGCTTTTGAATCTTACCTC 1265
QY 281 ----- 281
Db 1266 AGCTATGACCCCGGAGAGAAAGAAAGATTTGTAAACT---TCAGCCACGCA 1322
QY 299 ThrAsnTyrAsnGluLeuProLysAsnGlyLysGlySerThrArgLysGlyValAspHis 318
Db 1323 CTGGAGATAAAGGACTTAAAAAATGACTCTAAAGCACTGTGTAAAACTTGGACTCA 1382
QY 319 SerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSer 338
Db 1383 GTTCAGAAATTACCCCAAGGTGAACAAACCAAGTCAGAGACCGCTGGAGCTGATT 1442
QY 339 GlnGlyLeu----- 341
Db 1443 GCCAAGCTGAGAAAGGTGCTGATGTGTGCCAGTGTTCGACAGCTCCCGTTACCCGCG 1502
QY 342 ----- 342
Db 1503 ATACAGCCCAATTACCGTCCACTGCTTCCCTCGAGCTGATATCTCTCTCCAGCAAAAG 1562
QY 356 MetAspSerPheAsnGlyProSerHisGluAsn----- 366
Db 1563 CGAAAGCGTCTCTTCCACCCAGGAGAGAGAGAGCTGGATTCTTCTGGGCGCAGATG 1622
QY 367 ----- 378
Db 1623 AATTCAGATGCGAGGTGATTCTGTGTTCCAAAGTGTGCCTATCTCCCTAAATGATGACC 1682

QY 379 ---HisArgGln 381
Db 1683 TTGCACCAAGCAA 1694

RESULT 5
US-07-814-964-10
; Sequence 10, Application US/07814964
; Patent No. 5359047
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Pil, Pieter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kellett, Patti
; APPLICANT: Essigmann, John M.
; APPLICANT: Lippard, Stephen J.
; TITLE OF INVENTION: DNA Structure Specific Recognition
; TITLE OF INVENTION: Protein and Uses Therefor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/814,964
; FILING DATE: 19911226
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/539,906
; FILING DATE: 18-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-4787AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2384 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; IMMEDIATE SOURCE:
; CLONE: Drosophila SSRP - composite sequence
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 2
; MAP POSITION: 60A 1-4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 123...2291
US-07-814-964-10

Alignment Scores:
Pred. No.: 0.000795
Score: 138.50
Percent Similarity: 31.91%
Best Local Similarity: 21.20%
Query Match: 6.08%
DB: 1
Length: 2384
Matches: 99
Conservative: 50
Mismatch: 136
Indels: 182
Gaps: 23

US-09-700-696C-2 (1-430) x US-07-814-964-10 (1-2384)

QY 16 GlyLeuArgMetSerIleTyrProLysSerThrGly-AsnLysGlyPheGluAspGlyAs 35
Db 1187 GGAGCGAGGATTCATCTATATCCACAGCCACCGCTGCATATCGCTTTGAGGAG-----1241
QY 35 pAspAlaIleSerLysLeuHisAspGlnGluGluTyrGlyAla-----49
Db 1242 -----ATTAGTTCGTGAACACTTTCGCCGAGCGCGGATCCACGCGATCTTCGACTT 1294
QY 50 -----AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68
Db 1295 CGAAGTGCAGCTCAAGAACGGAACGTTCACATCTCTCTCCATC-----1340
QY 68 uLeuGlyGluGlnAsnLysGlnAsnThrProArgAsnValLeuAsnIleIleProAlaSe 88
Db 1341 -----GAGAAGGAGGAG-----1352
QY 88 rMetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAl 108
Db 1353 -----TATGCCAAGCTC-----1364
QY 108 aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLe 128
Db 1365 -----TTGCACTACAT 1375
QY 128 uLys-----HisLeuSerLysValLysLysIleProSerAspPheGluGlySe 144
Db 1376 CACACAGAGAGATTCATGTGTCCAGCAACATGGCGAAG-----GACAAGAG 1420
QY 144 rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164
Db 1421 CGGCTACAGAGAGCGT-----GACTTGGTGATTCGAGC-----AAGCAGAA 1462
QY 164 yGlnProPheLysAspIleProGly-----LysGlyGluAlaThrGlyProAspLeuGluGl 183
Db 1463 CGAACCAGATGCTATCTGGCTCGCTCAGCTGAGCGGAGGAGGAGGAGGAGCA 1522
QY 183 yAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
Db 1523 CGACGAT-----GGCGACTCGATGAAGAGATCCACGGATGAGGACTT 1564
QY 203 rLysLysProGlyTyrAsnGluIleProGluArgGluAsnGlyGlyAsnThrIleGl 223
Db 1565 C---AAGCCCAACGAGACGAGTCCGATGTGCGGAGGAGTATGACGCAACGTGGAGAG 1621
QY 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
Db 1622 TGATTCGAGCAT-----GACAGCGATGCTAGTGGC-----GGCGG 1657
QY 243 rAsnAspIleMetLysSerThrAsnPheLysGluLeuProGlyArgGluGlyAsnArgVa 263
Db 1658 AGCGGACAGCGCGCGCCCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAAA 1717
QY 263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProAlaPr 283
Db 1718 CGAGAAAAACACAG 1756
QY 283 oSerLysGluLysArgLysGluGlySer-----292
Db 1757 CTCGAAG 1816
QY 293 -----SerAspAlaAlaGluSer-----ThrAsnTyrAsnGluI 304
Db 1817 GCTGAACGACGCGCGAGAGATCAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1876
QY 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324
Db 1877 CGCAAG 1936
QY 324 aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344

1937 GCGGCCAAGGACAAAGCAGCGCTAC-----1961
QY 344 oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi 364
Db 1961 -----1961
QY 364 sGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSe 384
Db 1962 -----CAGCAGCAGATCGCAACACTACAAGCTGAAGCGGGCGGTGACAG 2005
QY 384 rThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArg-----GlnProHi 402
Db 2006 CGACACAGAGAGAGGT-----GGAAAGTCTCCAAAGAGCCCAAGACGAGCCTTC 2056
QY 402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413
Db 2057 TCATCCAAAGAGGGAATACCTCGGCGAGCGCTTCAAGAGCAAGGAGTACATTTCCGA 2116
QY 413 pAspSerSerGluSerSerAspSerGlySerSerGlu-----426
Db 2117 CGACGACTCCACGCTCCGACGACGAGAGAGACACGAGCCTGCCAAGAGAGAGCA 2176
QY 427 -----SerAspGlyAsp 430
Db 2177 GCGCCCATCCGACGCGGAT 2195

RESULT 6
US-08-258-442-10
Sequence 10, Application US/08258442
Patent No. 5670621
GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pil, Pieter M.
APPLICANT: Brown, Steven
APPLICANT: Keillett, Patti
APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,442
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2384 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

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; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; IMMEDIATE SOURCE:
; CLONE: Drosophila SRP - composite sequence
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 2
; MAP POSITION: 60A 1-4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 123..2291
US-08-258-442-10

Alignment Scores:
Pred. No.: 0.000795 Length: 2384
Score: 138.50 Matches: 99
Percent Similarity: 31.91% Conservative: 50
Best Local Similarity: 21.20% Mismatches: 136
Query Match: 6.08% Indels: 182
DB: 1 Gaps: 23

US-09-700-696C-2 (1-430) x US-08-258-442-10 (1-2384)
QY 16 GlyLeuArgMetSerIleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAs 35
DB 1187 GGAGCGAGATTCATCTATATCCACAGCCCGCTGCATATCCGCTTGAGGAG-----1241
QY 35 pAspAlaIleSerLysLeuHisAspGlnGluGlyGlyAla-----49
DB 1242 -----ATTAGTCTGTGAATTTGCCCGCAGCGCGGATCCACGGCATCTTCGACTT 1294
QY 50 ----AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68
DB 1295 CGAAGTGAGCTCCAGAACGCGACTGTTCATCTCTCTCCATC-----1340
QY 68 uLeuGlyGluGlnAsnLysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSe 88
DB 1341 -----GAGAAGGAGGAG-----1352
QY 88 rMetAsnTyrAlaLysAlaHisSerLysAspLysLysLysProGlnArgAspSerGlnAl 108
DB 1353 -----TATGCCAAGCTC-----1364
QY 108 aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLe 128
DB 1365 -----TTCGACTACAT 1375
QY 128 uLys-----HisLeuSerLysValLysLysLysLysProSerAspPheGluGlySe 144
DB 1376 CACACAGAGAAGTTGCATGTGCAGCAACATGGGCAAG-----GACAAGAG 1420
QY 144 rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164
DB 1421 CGGCTACAGGAGCTG--GACTTTGTGATTCGGAC-----AACGAGAA 1462
QY 164 yGlnProPheLysAspIleProGly--LysGlyGluAlaThrGlyProAspLeuGluGl 183
DB 1463 CGAACCATGATGCTCTATCTGCTCGCTCAAGCTGAGCGCGGAGGAGGAGGAGCA 1522
QY 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
DB 1523 CGACGAT-----GGCGATCGGATGAAGTCCACGGATGAGGACTT 1564
QY 203 rLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGl 223
DB 1565 C---AAGCCCAACAGAACAGTCCGATGTGGCCGAGGAGTATGACAGCAACGTGGAGAG 1621
QY 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
DB 1622 TGATTCGAGCAT-----GACAGCGATGCTAGTGGC-----GGCG 1657
QY 243 rAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsnArgVa 263

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DB 1658 AGCGACACGCGACGCGCCCAAGAAAGAGAGAGAGTCCCGAAGAAAGAGCAAA 1717
QY 263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProProAlaPr 283
DB 1718 GGAGAAAAAACACAAAGAGAGAGAGAGCAAAAG-----AAACC 1756
QY 283 oSerLysGluLysArgLysGluGlySer-----292
DB 1757 CTCCAAGAAAGAAAGAGACTCTGGCAAAACCCNAGCGCGCCACCACGGCTTTCATCTCTG 1816
QY 293 ----SerAspAlaAlaGluSer-----ThrAsnTyrAsnGluI 304
DB 1817 GCTGAACGACACGCGAGAGCATCAAGAGGAAAAATCCGGCATAAAAGGTTTACCGAGAT 1876
QY 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324
DB 1877 CGCCAAGAGGCGCGAGATGTGAAGAGAGTGAAGACAAAGTCCAAGTGGGAGATGC 1936
QY 324 aThrLeuAsnGlnLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344
DB 1937 GCGGCGCAAGGACACGACGCTAC-----1961
QY 344 oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi 364
DB 1961 -----1961
QY 364 sGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSe 384
DB 1962 -----CACGACGATGCGCAACTACAGCTGAAGCGGCGGTGACAG 2005
QY 384 rThrArgAsnLysGlyMetProGlnGlyLysGlySerThrGlyArg-----GlnProHi 402
DB 2006 CGACAACGAGAGAGGT-----GGAAGTCTCTCCAAAGACGCGCAACGCGAGCTTC 2056
QY 402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413
DB 2057 TCATCCAGAGAGCGAATACCTCGGCGAGCGCTTCAAGACGAGGATACATTTCCGA 2116
QY 413 pAspSerSerGluSerSerAspSerGlySerSerGlu-----426
DB 2117 CGACGACTCCACGAGCTCCGACGACGAGAGAGACACGAGCTGCCAAGAGAGAGCAA 2176
QY 427 -----SerAspGlyAsp 430
DB 2177 GCGCCCATCCGACGCGCAT 2195

RESULT 7
US-08-328-809-5
; Sequence 5, Application US/08328809
; Patent No. 5705334
; GENERAL INFORMATION:
; APPLICANT: Lippard, Stephen J.
; APPLICANT: Essigmann, John M.
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Pil, Pieter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kelleck, Patti
; TITLE OF INVENTION: Uses For DNA Structure-Specific
; TITLE OF INVENTION: Recognition Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,809

Alignment Scores:		
Pred. NO.:	0.000795	2394
Score:	138.50	99
Percent Similarity:	31.91%	Conservative: 136
Best Local Similarity:	21.20%	Mismatches: 50
Query Match:	6.08%	Indels: 182
DB:	1.	Gaps: 23

US-09-700-696C-2 (1-430) x US-08-328-809-5 (1-2384)

QY	16	GlyLeuArgMetSerIleTyrProLysSerThrGly-AsnLysGlyPheGluAspGlyAs	35
Db	1187	GGAGCGAGGAGTTCATCTATATCCACAGCCACCGCTGCATATCGGCTTTCAGGAG-	1241
QY	35	pAspAlaIleSerLysLeuHisaspGlnGluGluTyTGlyAla-	49
Db	1242	-----ATTAGTCTGTGAACTTTCGCCGAGCGCGGATCCACGGATCTTTCGACTT	1294
QY	50	---AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe	68
Db	1295	CGAAGTCACGCTCAAGAACCGAACTGTCACATCTCTCTCCCATC-	1340
QY	68	uLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSe	88
Db	1341	-----GAGAAGGAGGAG-	1352
QY	88	rMetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAl	108
Db	1353	-----TATGCCAGCTC-	1364
QY	108	aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLe	128
Db	1365	-----TTGCACTACAT	1375
QY	128	uLys-----HisLeuSerLysValLysIleProSerAspPheGluGlySe	144
Db	1376	CACACAGAAGAGTTGTCATGTCACACATCGGCCAAG-	1420
QY	144	iGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGl	164
Db	1421	CGGTATCAACGACTGTG--GACTTTGGTGGATTCCGAC-	1462

164	YcInProHeNyAsPilleProGly---	lysGlyGluAlaThrGlyProAspLeuGlucl	183
1463	CGAACCGATGCTATCTGCTGCTCGCTCAAGCTCAGGCGAGGAAAAGGAGGAGACGA	1522	
183	yyuAsPilleGInThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh	203	
1523	CGACGAT-----GGCGACTCGGTAAAGAGTCCACGATGAGACTT	1564	
203	rlYslySProGlyTyTyAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleG	223	
1565	C---ARGCCCAACGAAACGATCCGATGTGCCGAGGAGTATGACAGCAACGTGGAGAG	1621	
223	yThArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe	243	
1622	TGATTCGGACGAT-----GACACGATGCTAGTGC-----GGCGG	1657	
243	rAsnAsPilleMetGlySerThrAsnPhelySgluLeuProGlyArgGluGlyAsnArgVa	263	
1658	AGGCACACGCGCGGCCCAAGAAAAGAGAGAAGAGTCCGAGCAAGAAAGAGAAAAA	1717	
263	laspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyProProAlaPr	283	
1718	GGAGAAAAACACACAGGCAAGGAGACAAAG-----AAACC	1756	
283	oSerTySgluLysArgLysGluGlySer-----	292	
1757	CTCCAAAGAAAGAGGACTCTGCCAAACCCCAAGCGCCACACCGCTTTTCATGCTCTG	1816	
293	---SerAspAlaAlaGluSer-----ThrAsnTyAsnGluIle	304	
1817	GCTGAACGACACGCGCGAGAGCATCAGAGGAAAATCCGGGCATAAAGTTACCGAGAT	1876	
304	eProTysAsnGlyLysGlySerThArgLysGlyValAspHisSerAsnArgAsnGlnAl	324	
1877	CGCCAAAGAGGCGCGGAGATGTGGAAGGAGCTGAAGGACAAAGTCCCAAGTGGAGGATGC	1936	
324	aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr	344	
1937	GGCGGCCAAGGACACACGCGTAC-----	1961	
344	oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi	364	
1961	-----	1961	
364	sGluAsnIleIleThrHisGlyArgLysTyHisTyValProHisArgGlnAsnAsnSe	384	
1962	-----CACCACGAGATGCCCAACTACAAGCTTGAAGCGCGCGGTGCACAG	2005	
384	rThArgAsnLysGlyMetProGlnGlyLysGlySerTyArg-----GlnProHi	402	
2006	CGACAACGAGAGGGT-----GGAAAGTCTTCCAAGACGCGCAAGACGAGCTTC	2056	
402	sSerAsnArgArg-----PheSerSerArgArg-----ArgAs	413	
2057	TCCATCCAAAGAGCGGAATACCTCGGCGACGCGCTTCAAGAGCAAGAGGATACATTTCGGA	2116	
413	pAspSerSerGluSerSerAspSerGlySerSerSerGlu-----	426	
2117	CGAGCACTCCACAGTCCGACACACAGAGGACACAGCGCTGCCAAGAAAGAGACAA	2176	
427	-----SerAspGlyAsp	430	
2177	GCGCCCATCCGACGGGAT	2195	

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RESULT 8
US-08-866-840-5
; Sequence 5, Application US/08866840
; Patent No. 6475791
; GENERAL INFORMATION:
; APPLICANT: Lippard, Stephen J.
; APPLICANT: Essigmann, John M.
; APPLICANT: Donahue, Brian A.

```


APPLICANT: Toney, Jeffrey H.
 APPLICANT: Bruhn, Suzanne L.
 APPLICANT: Pil, Pieter M.
 APPLICANT: Brown, Steven
 APPLICANT: Kellett, Patti
 TITLE OF INVENTION: Uses For DNA Structure-Specific
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault
 STREET: 53 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/866,840
 FILING DATE: 02-JUN-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Fenton, Gillian M.
 REGISTRATION NUMBER: 36,508
 REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-248-7000
 TELEFAX: 617-248-7100
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2384 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Drosophila melanogaster
 IMMEDIATE SOURCE:
 CLONE: Drosophila SSRP - composite sequence
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: 2
 MAP POSITION: 60A 1-4
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 123..2291
 US-08-866-840-5

Alignment Scores:
 Pred. No.: 2384
 Length: 0.000795
 Matches: 99
 Score: 138.50
 Percent Similarity: 31.91%
 Conservativity: 50
 Mismatches: 136
 Best Local Similarity: 21.20%
 Indels: 182
 Query Match: 6.08%
 Gaps: 4
 DB:

US-09-700-696C-2 (1-430) x US-08-866-840-5 (1-2384)
 16 GlyLeuArgMetSerIleTyrProLysSerThrGly-AsnLysGlyPheGluAspGlyAs 35
 1187 GGAGCGAGATTCATCTATATCCACAGCCACCGCTGCATATCCGCTTTCAGGAG--- 1241
 35 pAspAlaIleSerLysLeuHisAspGlnGluGlyTyrGlyAla----- 49
 1242 -----ATTAGTTCGTGAACCTTTCGCCGAGCGCGGATCCACGCGATCTTTCGACTT 1294
 50 ----AlaLeuIleArgAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68
 1295 CGAAGTGCCTCAGAACGGNACTGTTTCATCTTCTCTCCATC----- 1340
 68 uLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIlelleProAlaSe 88

Db 2057 TCCATCAAGAGGCGAATACCTCGGCGAGCGGCTTCAAGACGAGGAGTACATTTCCGGA 2116
 Qy 413 pAspSerSerGluSerSerAspSerGlySerSerSerGlu----- 426
 Db 2117 CGAGACTCCACCGAGTCCGACGAGGAGGAGGACACGACGCTGCCAAGAGAGAGCA 2176
 Qy 427 -----SerAspGlyAsp 430
 Db 2177 GCCCCATCCGACGCGAT 2195

RESULT 9

PCT-US92-11107-10
 Sequence 10, Application PC/TUS9211107
 GENERAL INFORMATION:
 APPLICANT: Donahue, Brian A.
 APPLICANT: Toney, Jeffrey H.
 APPLICANT: Bruhn, Suzanne L.
 APPLICANT: Pil, Pieter M.
 APPLICANT: Brown, Steven
 APPLICANT: Kellest, Patti
 APPLICANT: Essigmann, John M.
 APPLICANT: Lippard, Stephen J.
 TITLE OF INVENTION: DNA Structure Specific Recognition
 TITLE OF INVENTION: Protein and Uses Therefor
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: 2 Millitia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/11107
 FILING DATE: 19921218

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/539,906
 FILING DATE: 18-JUN-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: MIT-4787AAA

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-861-6240
 TELEFAX: 617-861-9540
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2384 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Drosophila melanogaster
 IMMEDIATE SOURCE:
 CLONE: Drosophila SSRP - composite sequence
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: 2
 MAP POSITION: 60A 1-4
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 123..2291

Alignment Scores: 0.000795 Length: 2384
 Pred. No.: 138.50 Matches: 99
 Score:

Percent Similarity: 31.91% Conservative: 50
 Best Local Similarity: 21.20% Mismatches: 136
 Query Match: 6.08% Indels: 182
 DB: 5 Gaps: 23
 US-09-700-696C-2 (1-430) x PCT-US92-11107-10 (1-2384)
 Qy 16 GlyLeuArgMetSerIleTyProLysSerThrGly-AsnLysGlyPheGluAspGlyAs 35
 Db 1187 GGAGCGAGGATTATCATCTATATCCACAGCCCGCTGCATATCCGCTTTTGAGGAG----- 1241
 Qy 35 pAspAlaIleSerLysLeuHisAspGlnGluGluTyfGlyAla----- 49
 Db 1242 -----ATTAGTTCTGGAACCTTTCGCGGAGCGGCGATCCACGCGATCTTCGACTT 1294
 Qy 50 -----AlaLeuIleArgAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68
 Db 1295 CGAAGTGACGCTCAAGAACGGAACCTGTTTCACATCTTCTCTCCATC----- 1340
 Qy 68 uLeuGlyGluGlnAsnLysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSe 88
 Db 1341 -----GAGAAGGAGGAG----- 1352
 Qy 88 rMetAsnTyAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAl 108
 Db 1353 -----TATGCCAAGCTC----- 1364
 Qy 108 aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyfLe 128
 Db 1365 -----TTCCGACTACAT 1375
 Qy 128 uLys-----HisLeuSerLysValLysLysIleProSerAspPheGluGlySe 144
 Db 1376 CACACAGAGAAAGTTGTCATGTCCAGCAACATGGCGAAG-----GACAAGAG 1420
 Qy 144 rGlyTyThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164
 Db 1421 CGGCTACAAGGAGCTG---GACTTTGGTGATTTCGGAC-----AACGAGAA 1462
 Qy 164 yGlnProPheLysAspIleProGly---LysGlyGluAlaThrGlyProAspLeuGluGl 183
 Db 1463 CGAACCCAGATCCCTATCTCGCTCGCTCAAGCTGAGCGGAGGAGGAGGAGGAGCA 1522
 Qy 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
 Db 1523 CGACGAT-----GGCGACTCGGATGAAGAGTCCACGAGTACGAGACTT 1564
 Qy 203 rLysLysProGlyTyfAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGl 223
 Db 1565 C---AAGCCCAACGAGAACGATCCGATGTGCGCGAGGAGTATGACAGCAACGTGGAGAG 1621
 Qy 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
 Db 1622 TGATTCGGACGAT-----GACAGCGATGCTAGTGC-----GGCGG 1657
 Qy 243 rAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsnArgVa 263
 Db 1658 AGCGCACGCGACGGCGCCCAAGAAAAGAGAGAGAGAGTCCGAGAGAGAGAGAGAAA 1717
 Qy 263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyfProProAlaPr 283
 Db 1718 GGAGAAAAAACACAG 1756
 Qy 283 oSerLysGluLysArgLysGluGlySer----- 292
 Db 1757 CTCACAGAGAGAGAGAGAGACTCTCGGCAACCCAAAGCGCGCCACCACCGCTTTCATGCTCG 1816
 Qy 293 -----SerAspAlaAlaGluSer-----ThrAsnTyfAsnGluI 304
 Db 1817 GCTGACGACACACGCGCGAGAGCATCAAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAT 1876
 Qy 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324

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Db 1877 CGCCAAAGAGGGCGGAGATGCTGAAGAGCTGAAGCAAGTCCAGTGGGAGATGC 1936
Qy 324 aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344
Db 1937 GCGCGCCAAAGCAAGCAGCGCTAC-----1961
Qy 344 oSerArgGlyLeuAspAsnGluLysAsnGluMetAspSerPheAsnGlyProSerHi 364
Db 1961 -----1961
Qy 364 sGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSe 384
Db 1962 -----CAGCAGGAGATCGGCAACTACAGCTCAAGCGGCGGTGACAG 2005
Qy 384 rThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArg-----GlnProHi 402
Db 2006 CGACAACGAGAGGGT-----GGAAATGCTCCAAAGAGCGCAAGCGGAGCTTC 2056
Qy 402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413
Db 2057 TCCATCCAAAGAGCGGAATACCTCGGCGAGCGGCTTCAAGAGCAAGGAGTACATTTCGGA 2116
Qy 413 pAspSerSerGluSerAspSerGlySerSerGlu-----426
Db 2117 CGAGGACTCCACAGCTCCGACGACGAGAGGACACAGCGCTGCCAAGAGAGAGCAA 2176
Qy 427 -----SerAspGlyAsp 430
Db 2177 GCCCCCATCCGAGCGCAT 2195

RESULT 10
US-08-320-559-27
; Sequence 27, Application US/08320559
; Patent No. 5633135
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
; TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
; TITLE OF INVENTION: All-1 Region
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/320,559
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/062,443
; FILING DATE: 14 MAY 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/971,094
; FILING DATE: 30-OCT-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/888,830
; FILING DATE: 27-MAY-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/805,093
; FILING DATE: 11-DEC-91
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229

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; REFERENCE/DOCKET NUMBER: TJU-0855
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9370 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 469..4032
; US-08-320-559-27

Alignment Scores:
Pred. No.: 0.0081 Length: 9370
Score: 137.00 Matches: 100
Percent Similarity: 34.70% Conservatives: 61
Best Local Similarity: 21.55% Mismatches: 192
Query Match: 6.01% Indels: 113
DB: 1 Gaps: 17

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Qy 37 AlaIleSerLysLeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnMet 56
Db 1938 GCAGCTGGACACTGGCTGACCAAGTCAGCCAGCAGCTGGCCACCAGAGGGGCCAG 1997
Qy 57 GlnHisIleMetGlyProValThrAlaIleLysLeuGlyGluGluAsnLysGluAsn 76
Db 1998 GAGCAC---AGAGCCCCCAGCGCGCACCCAGAGTAGGAGCAGCAGCAGTGCAC 2054
Qy 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
Db 2055 GAGTC-AGGAGCATCTGATCCAAAGATCTCTCCC-----CTAAAGCT 2098
Qy 95 HisSerLysAspLysLysLysProGlnArg-----AspSerGlnAlaGln 109
Db 2099 CC-AGCAAGCCCCCGGCGCCACCCGGAAGCCCCCAGCGGAGAGGAGGTGTGAG 2157
Qy 110 LysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLeuLys 129
Db 2158 AGTCTCCGGCAGCAGGAGGAGCCCCCAAGAGGCAACCGTTGGACCAACCAACCCAAA 2217
Qy 130 HisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeu 149
Db 2218 -----AAACTGTCAAGGCTCTGCGCGGCGAGGTTCAAGGAGCAGCCTG 2262
Qy 150 GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAsp 169
Db 2263 CAGGGGAAAGGAGGAGCGAGGCTTTCTTCCTATGCTCCCGAGACAGACTTCCAAAGAC 2322
Qy 170 IlePro-----GlyLysGlyGlu-----175
Db 2323 AAGCCCCAAGTGAAGAGCAAGAGGAGCGGCCCGCGGCGCAGCAAGCAAGCAAGCCAAAGCCA 2382
Qy 176 AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195
Db 2383 GCAGTCCCTCCCTCCAGTGAAGAGCAAGAGCACAAGAGTCCCTCCCTGCCCTCTTAAG 2442
Qy 196 AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr-----208
Db 2443 GCTCTCTCAGGCCCAAGACCCCGAAGGACAATGTTGGAGCAGGAGCCCTGAGCATT 2502
Qy 209 -----AsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
Db 2503 GCTCTTGTTCCTCGTACGAGGAGCGGCGCCCAACCCAGTCAGTGGCGGCGGAGGAGCT 2562
Qy 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
Db 2563 AGTGGCTGCGGCCCAAGCCGCTGTGTGTCAGGAGGAGCAGCGCGCAAGACAGACTCCCAT 2622

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Prod. No.:	0.00813	Length:	9391
Score:	137.00	Matches:	100
Percent Similarity:	34.70%	Conservative:	61
Best Local Similarity:	21.55%	Mismatches:	192
Query Match:	6.01%	Indels:	113
DB:	1	Gaps:	17

US-09-700-696C-2 (1-430) x US-08-320-559-25 (1-9391)

QY	37	AlaIleSerLysLeuHisAspGlnGluThrGlyAlaAlaLeuIleAsnMet	56
DB	1959	CGAGTGGACAACTGGCTGACCAAGTCAAGCAGCGCTGCCACACAGAGGCCGCCAG	2018
QY	57	GlnHisIleMetGlyProValThrAlaIleLysLeuGluGluAsnLysGluAsn	76
DB	2019	GAGCAC--AGAGCCCCAGCGCGCCACCCAGAGAGTAAGGGCAGCAGCAGCGACGTC	2075
QY	77	ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla	94
DB	2076	GAGTC-AGAGCATTCTGAATCCAAAGATCTCTCC-----CTAAAGCT	2119
QY	95	HisSerLysAspLysLysProGlnArg-----AspSerGlnAlaGln	109
DB	2120	CC-AGCAAGACCCCGCGGCCCCACCCGAAAGCCCCACCCCGGAAAGAGAGCTGTG	2178
QY	110	LysSerProValLysSerLysThrHisArgIleGlnHisAsnIleAspTyrLeuLys	129
DB	2179	AACTCTCCGGCAGCAGGAGCCGCCCAAGAGGCAACCGTTGGAAACCAACACCCAAA	2238
QY	130	HisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeu	149
DB	2239	-----AACTGTCAAGGCTCTGCGCGGCGAGTTCACGACCCAGCGCTG	2283
QY	150	GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAsp	169
DB	2284	CAGGGGAAAGGAGCCAGGGCTTCTTCTTATGCTCCGAGACCACTTCCAAAGAC	2343
QY	170	IlePro-----GlyLysGlyGlu-----	175
DB	2344	AAGCCCAAGTGAAGACGAAAGAGCGCGCGCGCGCAGCAAGCAAGCAACCCAAAGCCA	2403
QY	176	AlaThrGlyProAspLeuGluGlyAspIleGlnThrGlyPheAlaGlyProSerGlu	195
DB	2404	CGAGTCCCCCTCCAGTCAGTGAAGAAGAACCAAGAGCTCCCTCCCTGCGCCCTCTAAG	2463
QY	196	AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr---	208
DB	2464	GCTCTCTAGGCCAGAACCCCGGAGGACAAATGTGGAGGACAGGACCCCTGAGCACTTT	2523
QY	209	-----AsnGluIleProGluArgGluGluAsnGlyAsnThr	221
DB	2524	GCTCTGTTCCTGACTGAGACGACCGGCCACCCACCCAGTGGCGCGGCGAGGAGCT	2583
QY	222	IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu	241
DB	2584	AGTGGTCCGCGCAACCGCTGGTTCAGGAGGACGCGGCAAGACAGACTCCCATTTG	2643
QY	242	GlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsn	261
DB	2644	CCTTTGAGAGACCAAGGCTGTCTCACCGCTCAGGAGCACTCTCCCCCAAGAGCTTG	2703
QY	262	ArgVal-----AspAlaGlySerGlnAsnAla	270
DB	2704	ATGTTGAAGATCACCTAGACCTGTCTCTCGATACCCAGCTCCCGGGAAGGGAGC	2763
QY	271	HisGlnGlyValGluPheHisTyrProProAlaProSerLysGluLysArgLysGlu	290
DB	2764	CGCCAGGAGAAACGACAGAGATAAACAGCGCGCGGAGGAAGACAGCTCTTGAGAG	2823
QY	291	GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGlyGly	310
DB	2824	AGGAGCTCACAGCTCA-----AGCAAGTTCGCCCAAAAGAGAAAGGCT	2868

QY	311	SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln	330
DB	2869	GAAGCAGAAAGAGACTGTGAT-----AACAGAAATC	2901
QY	331	ArgPheProSerLysGlyLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsn	350
DB	2902	AGA-----CTGGAGAAG	2913
QY	351	GluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleThr---	369
DB	2914	GAATCAATCAGACTCATCTTCATCTCCACAAAGAAATCTTAAACAAAG	2973
QY	370	-----HisGlyArgLysTyrHisTyrValProHisArgGlnAsn	382
DB	2974	CCCTCCAGCCCTCTCAGACTCTCAAGAAAGAAATGCTCCCGCCGCCACCGGTGTC	3033
QY	383	AsnSerThrArgAsnLysGlyMetProGlnGlyLysSer-----	396
DB	3034	TGTCCTCCAGAGACCCAGCCAGCTGCTAAAGAGGTCAAGGGTCAAGGGGGAAGCAGACAC	3093
QY	397	TrpGlyArgGlnPro-----HisSerAsnArgPheSerSer	409
DB	3094	TGTGCCAGGACCTCTCCAAAGTGCACAGTACCAAGAGCAACCAAGAGACTCTTCC	3153
QY	410	ArgArgAspAspSerSerGluSerSerAspSerGlySerSerSerGlu-----	426
DB	3154	ATTCCAGCAGAGAGAGTAGAGGGGAGGCTCCAGAGACTCTCGGAGCAACAGGGT	3213
QY	427	SerAspGlyAsp	430
DB	3214	TCTTCCGGAGAT	3225

RESULT 14

US-08-545-860D-25

Sequence 25, Application US/08545860D

Patent No. 6040140

GENERAL INFORMATION:

APPLICANT: Crocco, Carlo

APPLICANT: Canaani, Eli

TITLE OF INVENTION: Diagnostics, Therapeutics and Methods

TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias

TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS: 94

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &

ADDRESS: No. 6040140ris

STREET: One Liberty Place, 46th floor

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/545,860D

FILING DATE: 07-MAR-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/04496

FILING DATE: 22-APR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10930

FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/327,392

FILING DATE: 19-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/320,559

FILING DATE: 11-OCT-1994

PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: US 08/062,443
/ FILING DATE: 14-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/971,094
/ FILING DATE: 30-OCT-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/888,839
/ FILING DATE: 27-MAY-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/805,093
/ FILING DATE: 11-DEC-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Deluca Esq., Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: TJU-1262
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 25:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9391 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 421...4053
/ US-08-545-860D-25

Alignment Scores:
Pred. No.: 0.00813 Length: 9391
Score: 137.00 Matches: 100
Percent Similarity: 34.70% Conservative: 61
Best Local Similarity: 21.55% Mismatches: 132
Query Match: 6.01% Indels: 113
DB: 3 Gaps: 17

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Db 2019 GAGCAC---AGAGCCCGGCGGCGCCAGAGAGTAAAGGCGAGCGAGCGAGTCCAC 2075
QY 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
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QY 95 HisSerLysAspLysLysLysProGlnArg-----AspSerGlnAlaGln 109
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QY 110 LysSerProValLysSerLysSerThrHisArgIleGlnHisIleAspTyrLeuLys 129
Db 2179 AAGTCTCCGCGACAGCAGAGAGCCCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2238
QY 130 HisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeu 149
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QY 150 GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAsp 169
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QY 170 IlePro-----GlyLysGlyGlu----- 175
Db 2344 AAGCCCAAGGTGAAGACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2403
QY 176 AlaThrGlyProAspLeuGluGlyAspIleGlnThrGlyPheAlaGlyProSerGlu 195
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/ APPLICATION NUMBER: US 08/062,443
/ FILING DATE: 14-MAY-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/971,094
/ FILING DATE: 30-OCT-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/888,839
/ FILING DATE: 27-MAY-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/805,093
/ FILING DATE: 11-DEC-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Deluca Esq., Mark
/ REGISTRATION NUMBER: 33,229
/ REFERENCE/DOCKET NUMBER: TJU-1262
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 568-3100
/ TELEFAX: (215) 568-3439
/ INFORMATION FOR SEQ ID NO: 25:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 9391 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 421...4053
/ US-08-545-860D-25

RESULT 15
PCT-US94-04496-25
; Sequence 25, Application PC/TUS9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaan, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
; NUMBER OF SEQUENCES: 86

```


CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
 ADDRESSEE: Norris
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04496
 FILING DATE:

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Deluca Esq., Mark
 REGISTRATION NUMBER: 33,229
 REFERENCE/DOCKET NUMBER: TTU-1242
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9391 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 421..4053
 PCT-US94-04496-25

Alignment Scores:
 Pred. No.: 0.00813 Length: 9391
 Score: 137.00 Matches: 100
 Percent Similarity: 34.70% Conservative: 61
 Best Local Similarity: 21.55% Mismatches: 192
 Query Match: 6.01% Indels: 113
 DB: 5 Gaps: 17

US-09-700-696C-2 (1-430) x PCT-US94-04496-25 (1-9391)

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 DB 1959 GCAGCTGGCAACTGCTGCTACCAAGTCAGCCAGCCAGCTGGCGCCACAGAGGCCCCAG 2018
 QY 57 GlnHisIleMetGlyProValThrAlaIleLysLeuGlyGluGluAsnLysGluAsn 76
 DB 2019 GAGCAC---AGAGCCCCCAGCGGCCACCCAGAGAGTAGGAGGCGACGAGCGTCCAC 2075
 QY 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
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 Job time : 182 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Run on: March 29, 2004, 01:33:17 ; Search time 451 seconds

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Searched: 2455946 seqs, 1861504846 residues

Total number of hits satisfying chosen parameters: 4917892

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR_SCORE=ext -THR_WAX=100
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Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match Length DB ID Description

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3	2276	99.9	1662	14	US-10-311-840-3	Sequence 3, Appli
4	2276	99.9	1876	10	US-09-794-422-33	Sequence 33, Appli
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6	2276	99.9	2013	12	US-10-438-181A-26	Sequence 26, Appli
7	2276	99.9	2019	10	US-09-794-422-5	Sequence 5, Appli
8	2276	99.9	2112	10	US-09-794-422-7	Sequence 7, Appli
9	993.5	43.2	1682	10	US-09-794-422-3	Sequence 3, Appli
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13	148	6.5	3045	15	US-10-108-260A-1338	Sequence 1338, Ap
14	148	6.5	4985	12	US-10-210-172-65	Sequence 65, Appli
15	148	6.5	5721	9	US-09-785-770A-15	Sequence 15, Appli
16	148	6.5	5964	12	US-10-210-172-63	Sequence 63, Appli
17	148	6.5	8121	9	US-09-785-770A-14	Sequence 14, Appli
18	140	6.1	2673	14	US-10-153-668-301	Sequence 301, App
19	140	6.1	4839	14	US-10-101-510-396	Sequence 396, App
20	139	6.1	2381	15	US-10-104-047-1415	Sequence 1415, Ap
21	139	6.1	35465	14	US-10-161-572-6	Sequence 6, Appli
22	139	6.1	36991	14	US-10-161-572-8	Sequence 8, Appli
23	137	6.0	3668	15	US-10-108-260A-1304	Sequence 1304, Ap
24	137	6.0	9390	14	US-10-205-823-263	Sequence 263, App
25	135	5.9	5406	12	US-10-615-383-1	Sequence 1, Appli
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28	134	5.9	1446	14	US-10-156-761-4465	Sequence 4465, Ap
29	134	5.9	2254	14	US-10-198-846-13929	Sequence 13929, A
30	134	5.9	9025608	14	US-10-156-761-1	Sequence 1, Appli
31	133.5	5.9	1960	9	US-09-864-761-4620	Sequence 4620, Ap
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33	133	5.8	3876	12	US-10-312-353-68	Sequence 68, Appli
34	132.5	5.8	2594	15	US-10-108-260A-355	Sequence 355, App
35	132	5.8	4899	12	US-10-282-122A-34253	Sequence 34253, A
36	131.5	5.8	2930	12	US-10-240-425-1324	Sequence 1324, Ap
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38	131	5.7	2025	9	US-09-834-975-822	Sequence 822, App
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44	130.5	5.7	3316	14	US-10-133-013-166	Sequence 166, App
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ALIGNMENTS

RESULT 1

US-10-438-181A-1

Sequence 1, Application US/10438181A

Publication No. US20040053389A1

GENERAL INFORMATION:

APPLICANT: Rowe, Peter Stanley Nicola

TITLE OF INVENTION: NO. US20040053389A1el Polypeptide Hormone-Phosphatonin

FILE REFERENCE: BEAR-005CIP

CURRENT APPLICATION NUMBER: US/10/438,181A

CURRENT FILING DATE: 2003-05-13

PRIOR FILING DATE: 2002-04-25

PRIOR FILING DATE: 2002-04-25

PRIOR APPLICATION NUMBER: 09/434,185

PRIOR FILING DATE: 1999-11-04

PRIOR APPLICATION NUMBER: PCT/EP99/03403

PRIOR FILING DATE: 1999-05-18

PRIOR APPLICATION NUMBER: GB 9810681.8

PRIOR FILING DATE: 1998-05-18

PRIOR APPLICATION NUMBER: GB 9819387.3

PRIOR FILING DATE: 1998-09-04

NUMBER OF SEQ ID NOS: 55

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 1655

TYPE: DNA
ORGANISM: Homo sapien
US-10-438-181A-1

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Pred. No.: 1,01e-214 Length: 1655
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-700-696C-2 (1-430) x US-10-438-181A-1 (1-1655)

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QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
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DB 841 CCTGCACCTTCAAAAGAGAGAAAGAAAGAGGAGGAGTGTGATGATGCTGAAGTACCAAC 900

QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
DB 901 TATAATGAAATTCCTAAAAATGCAAGGCACTACAGAAAGGGTGTAGATCATTTCTAAT 960
QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
DB 961 AGGAACCAAGCAACCTTAATGAAAAACAAGGTTTCTTAGTAGGGCAAAAGTCAGGCG 1020
QY 341 LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn 360
DB 1021 CTGCCCATTCCTTCTCGTGTCTTGATAATGAATCAAAAGCAAAATGATGATTCCTTTAAT 1080
QY 361 GlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
DB 1081 GGCCCGAGTCAGAGATATATAACACATGGCAGAAATATCATTTATGACCCACAGA 1140
QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysSerTrpGlyArgGln 400
DB 1141 CAAAATAATTTCTACCGGAATAGGGTATGCCCAAGGGAAAGGCTCCTGGGGTAGACAA 1200
QY 401 ProHisSerAsnArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
DB 1201 CCCATTCACAGAGAGGTTTAGTTCCTGAGAGGGATGACAGTAGTAGTCTGATCTGAC 1260
QY 421 SerGlySerSerGluSerAspGlyAsp 430
DB 1261 AGTGGCAGTTCAAGTGAGAGCGATGGTGAC 1290

RESULT 2

US-10-311-840-2
Sequence 2, Application US/10311840
Publication No. US20030175808A1
GENERAL INFORMATION:
APPLICANT: KUROKAWA, Tomofumi
APPLICANT: YAMADA, Takao
APPLICANT: MORIMOTO, Shigeto
TITLE OF INVENTION: No. US20030175808A1: Protein and its DNA
FILE REFERENCE: 2738USOP
CURRENT APPLICATION NUMBER: US/10/311,840
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: PCT/JP01/05263
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: JP 2000-191088
PRIOR FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
LENGTH: 1575
TYPE: DNA
ORGANISM: Human
US-10-311-840-2

Alignment Scores:
Pred. No.: 1.87e-214 Length: 1575
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 14 Gaps: 0

US-09-700-696C-2 (1-430) x US-10-311-840-2 (1-1575)

QY 1 ValAsnLysGluTyrSerHisSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
DB 286 CTGAATAAAGAAATATAGTATCAGTAAACAAAGAGAAATCTCAAAATGGGCTGAGGATGCA 345
QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
DB 346 ATTTATCTTAAGTCACTGGGAAATAAGGTTTGGAGTGGAGATGATGCTATCAGCAA 405
QY 41 LeuHisAspGlnGluGluTyrGlyAlaAlaLeuIleArgAsnMetGlnHisIleMet 60
DB 406 CTACATGACCAAGAGAGATATGGCGAGCTCTCATCAGAAATAACATGCAACATATAATG 465

QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluAsnLysGluAsnThrProArgAsn 80
Db 466 GGGCCAGTGAATCGGATTAACTCTCGGGGAGAGAAACAAAGAGAACACACCTAGGAAT 525
QY 81 ValLeuAsnIleLeuProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 526 GTTCTAAACATAATCCCAAGCAAGTATGAATATGCTAAAGCAGACACTCGAAGGATAAAAG 585
QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 586 AAGCCTCAAGAGATTCACAGCCAGAAAGTCAAGTAAAGCAAAAGCAACCCATCGT 645
QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db 646 ATTCAACACAACTTACCTTAAACATCTCTCAAAAGTCAAAATAATCCCAAGTAT 705
QY 141 PheGluGlySerGlyTyrThrAspLeuGlnArgGlyAspAsnAspIleSerProPhe 160
Db 706 TTTGAAGGAGCGGTTATACAGATCTTCAAGAGAGGGGCAATGATATATCTCTTC 765
QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 766 AGTGGGACGGCCAACTTTTAAGCACATCTCTGTTAAAGGAGAAAGCTACTGCTCTGAC 825
QY 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 826 CTAGAAGGCAAGATATTCACACAGGTTTGCAGGCCCAAGTGAAGTCAAGTACTCAT 885
QY 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyLys 220
Db 886 CTTGACACAAAAGCCAGTTATATGATAGATCCCAAGAGAGAGAAATGGTGGAAAT 945
QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
Db 945 ACCATTGGAACAGGATGAAATCGAAAGAGAGGAGATGCTGTTGATGTCAGCCTTGA 1005
QY 241 GluGlySerAsnAspIleMetGlySerThrAsnAspLysGluLeuProGlyArgGluGly 260
Db 1006 GAGGCGAGCAACGATATATGCTGCTACCAATTTTAAGGAGCTCCCTGGAAGAGAGA 1065
QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
Db 1066 AACAGAGTGATCTCGCAGCCAAAATGCTCCACAGGGAAGGTTGAGTTTCAATACCT 1125
QY 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
Db 1126 CCTGCACCTTCAAAAGAGAAAGAAAGAGAGGAGTGTGATGATGATGATGATGATGAT 1185
QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1186 TATAATGAAATCTCTAAATGCGCAAGGAGGAGTACCAAGGAGGAGGAGTATCTTAAAT 1245
QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1246 AGGAACCAAGCAACCTTAAATGAAACAAAGGTTTCTAGTAAAGGCAAAAGTCAAGG 1305
QY 341 LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn 360
Db 1306 CTGCCATTCCTTCTCGTCTTGATATGAAATCAAAACCAAAATGGAATGCTTCTTAAAT 1365
QY 361 GlyProSerHisGluAsnIleLeuThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1366 GGCCCCAGTATGAGATATAAATACACATGGGAGAAATATCATATGATGATGATGATGAT 1425
QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTrpGlyArgGln 400
Db 1426 CAATATATCTACACGGAATAAGGATATGCCACAGGGAAGGCTCTCTGGGATAGACAA 1485
QY 401 ProHisSerAsnArgArgPheSerArgArgArgAspAspSerSerGluSerSerAsp 420
Db 1486 CCCCATCTTCAACAGGAGGTTTAGTCTCCGCTAGAGGAGGATGACAGTATGATCATCTGAC 1545

QY 421 SerGlySerSerSerGluSerAspGlyAsp 430
Db 1546 AGTGGCAGTTCAAGTCAGAGCGATGGTGAC 1575

RESULT 3

US-10-311-840-3
; Sequence 3, Application US/10311840
; Publication No. US20030175808A1
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tomofumi
; APPLICANT: YAMADA, Takao
; APPLICANT: MORIMOTO, Shigeto
; TITLE OF INVENTION: No. US20030175808A1el Protein and its DNA
; FILE REFERENCE: 273USOP
; CURRENT APPLICATION NUMBER: US/10/311,840
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/JP01/05263
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191088
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-10-311-840-3

Alignment Scores:
Pred. No.: 2,01e-214 Length: 1662
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
Gaps: 0

US-09-700-696C-2 (1-430) x US-10-311-840-3 (1-1662)

QY 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisShengLysLeuArgMetSer 20
Db 293 CTGAATAAAGATATATAGTATATCACTAAAGAGAGAAATCACTCACAATGGCCCTGAGATGTCA 352
QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
Db 353 ATTTATCTTAAGTCACTGGGATTAAGGGTTTGAGGATGGAGATGATGATCAACGAAA 412
QY 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMet 60
Db 413 CTACATGACCAAGAGAAATATGGCCAGCTCTCATCAGAAATAACATGCAACATATAATG 472
QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluAsnLysGluAsnThrProArgAsn 80
Db 473 GGGCCAGTGAATCGGATTAAGTCTCTGGGGAGAGAAACAAAGAGAACACACCTAGGAAT 532
QY 81 ValLeuAsnIleLeuProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 533 GTTCTAAACATAATCCCAAGCAAGTATGATATATGCTAAAGCAGACACTGGAAGGATAAAAG 592
QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 593 AAGCCTCAAGAGATTCACAGCCAGAAAGTCCAGTAAAGCAAAAGCAACCCATCGT 652
QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db 653 ATTCAACACAACTTACTACTTAAACATCTCTCAAAAGTCAAAATAATCCCAAGTAT 712
QY 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
Db 713 TTTGAAGGAGCGGTTATACAGATCTTCAAGAGAGAGGGGCAATGATATATCTCTCTTC 772
QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 773 AGTGGGAGCGGCAACCTTTTAAAGACATCTCTGTTAAGGAGAGAGTACTGCTCTGCTGAC 832

181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 833 CTAGAAGGCAAGATATTCAACAGGGTTTCAGGCCCAAGTGAAGCTGAGACTCAT 892

201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluGluGluGluGlyAsn 220
Db 893 CTTCGACACAAAAGCCAGGTTATATGAGATCCAGAGAGAGAGAAATGGTGGAAT 952

221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
Db 953 ACCATTGGAACTAGGATGAACTCGGAAAGAGGAGAGATGCTGTTGATGTCAGCCCTTGA 1012

241 GluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGluGluGly 260
Db 1013 GAGGCGAGCAACGATATCATGGTGTAGTACCAATTTTAAGGAGCTCCCTGGAGAGAGGA 1072

261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyValGluPheHisTyrPro 280
Db 1073 ACAGAGTGGATGCTGGAGCCMAATGCTCCACAGGAGGAGGTGAGTTTCATTACCT 1132

281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
Db 1133 CTGCACCCCTCAAAAGAGAGAAAGAAAGAGGAGGAGTGTGTCAGCTGAAAGTACCAAC 1192

301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1193 TATAATGAATTCCTTAAATGSCAAAGGAGGAGTACCAAGAGGAGGTGATCTTCTAAT 1252

321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1253 AGGAACCAAGCAACCTTAAATGAAAGAAAGAGGTTTCTAGTAAAGGCAAAAGTCAGGCG 1312

341 LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn 360
Db 1313 CTGCCATTCCTTCTCGTGTCTTGATATGTAATCAAAACGAAATGATTCCTTTAAT 1372

361 GlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1373 GGCCCCAGTCATGAGAATATAATAACACATGGCAGAGAAATATCATTTATGCCCCACAGA 1432

381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGln 400
Db 1433 CAAATTAATTTCTACAGGAATAAGGGTATGCCCAAGGAGGAGGCTCCTGGGGTAGACAA 1492

401 ProHisSerAsnArgArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
Db 1493 CCCATTCCACAGGAGGTTTGTTCCTCGTAGAAGGAGTACAGATGATGATGATCTGAC 1552

421 SerGlySerSerSerGluSerAspGlyAsp 430
Db 1553 AGTGGCAGTTCAAGTGAGCGGATGGTGAC 1582

RESULT 4

US-09-794-422-33
; Sequence 33 Application US/09794422
; Publication No. US2003016239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 1876

TYPE: DNA
ORGANISM: Homo sapiens
US-09-794-422-33

Alignment Scores: 2,35e-214 Length: 1876
Pred. No.: 2276.00 Matches: 429
Score: 100.00% Conservative: 1
Percent Similarity: 99.77% Mismatches: 0
Best Local Similarity: 99.87% Indels: 0
Query Match: 19 Gaps: 0
DB: 10

US-09-700-696C-2 (1-430) x US-09-794-422-33 (1-1876)

Qy 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisGlnGlyLeuArgMetSer 20
Db 238 CTGAATAAAGATATAGTATCAGTAAAGAGAGATACTCACAATGCCTGAGGATGTCA 297

Qy 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
Db 298 ATTATCTCACTCACTGCGAATAAAGGTTTGAGGATGGAGATGATGCTATCAGCAA 357

Qy 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMet 60
Db 358 CTACATGACCAAGAAGAAATATGGCGAGCTCTCATCAGAAATTAACATGCAACATATAATG 417

Qy 61 GlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80
Db 418 GGGCCAGTGACTGGATTAACCTCTCGGGGAGAGAAACAAAGAGAACACACCTAGGAAT 477

Qy 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 478 GTTCTAAACATAATCCCGCAAGATATGAAATATGCTAAAGCACACTCGAAGAGATAAAAG 537

Qy 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 538 AAGCCTCAAGAGAGATCCCAAGCCCAAGAAAGTCCAGTAAAGCAAAAGCACACCTATCGT 597

Qy 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db 598 ATTCAACACACAACTTGACTACCTAAACATCTCTCAAAAGTCAAAAAATCCCAAGTAT 657

Qy 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
Db 658 TTTCAAGAGCGCGTTTATACAGATCTTCAAGAGAGAGGGGACAAATGATATATCTCTTTC 717

Qy 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 718 AGTGGGAGCGCCCAACCTTTTAAGGACATTCCTGTAAAGAGAGAGCTACTGCTCTGAC 777

Qy 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 778 CTAGAAGGCAAGATATATCAACAGGGTTTCAGGCCCAAGTGAAGCTGAGAGTACTCAT 837

Qy 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn 220
Db 838 CTTCGACACAAAAGCCAGGTTTAAATGAGATCCAGAGAGAGAGAGAAATGGTGAAT 897

Qy 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
Db 898 ACCATTGGAACTAGGATGAACTCGGAAAGAGGAGAGATGCTGTTGATGTCAGCCTTGA 957

Qy 241 GluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGly 260
Db 958 GAGGCGAGCAACGATATCATGGTGTAGTACCAATTTTAAGGAGCTCCCTGGAGAGAGGA 1017

Qy 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
Db 1018 AACAGAGTGGATGCTGGCAGCAAAATGCTCACCAGAGGAGGTTGATGTTTCAATACCT 1077

Qy 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
Db 1078 CTTGCACCTTCAAGAGAGAAAGAAAGAGGAGGAGTGTGATGTCAGCTGAAAGTACCAAC 1137

QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
 Db 1138 TATAATGAATTCCTAAATAATGCGAAGCAGTACCAGAAAGGGGTAGATCATTTCTAAT 1197
 QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
 Db 1198 AGGAACCAAGCAACCTTAATGAAAACAAGAAGTTCTCTAGTAGGGCAAGTACAGGC 1257
 QY 341 LeuProIleProSerArgGlyLeuAspAsnGluLysLysAsnGluMetAspSerPheAsn 360
 Db 1258 CTGCCCATTCCTTCCTGCTGCTTCGATATGAATCAAAACGAAATGGATTCCTTTAAT 1317
 QY 361 GlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
 Db 1318 GCGCCCAAGTCATGAGATATATACACATGCGAGAAATATCATTAATGTACCCACAGA 1377
 QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGln 400
 Db 1378 CAAATAAATCTACACGAATAAGGATGATCCACAAAGGAAAGGCTCCTGGGGTAGACAA 1437
 QY 401 ProHisSerAsnArgArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
 Db 1438 CCCATTCACACAGGAGGTTTGTTCCTCCGTAGAAGGATGACAGTAGTGAGTCATCTGAC 1497
 QY 421 SerGlySerSerSerGluSerAspGlyAsp 430
 Db 1498 AGTGGCAGTTCAAGTGAGAGCGATGGTGAC 1527
 RESULT 5
 US-09-794-422-45
 ; Sequence 45, Application US/09794422
 ; Publication No. US20030166239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Thomas A.
 ; APPLICANT: De Wet, Jeffrey R.
 ; APPLICANT: Gowen, Lori C.
 ; APPLICANT: Hames, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins
 ; FILE REFERENCE: PC10445
 ; CURRENT APPLICATION NUMBER: US/09/794,422
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 60/185,617
 ; PRIOR FILING DATE: 2000-02-29
 ; PRIOR APPLICATION NUMBER: 60/234,500
 ; PRIOR FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 45
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-794-422-45

Alignment Scores:
 Pred. No.: 2,516-214 Length: 1369
 Score: 2276.00 Matches: 429
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.77% Mismatches: 0
 Query Match: 99.87% Indels: 0
 DB: 10 Gaps: 0
 US-09-700-696c-2 (1-430) x US-09-794-422-45 (1-1969)
 QY 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
 Db 331 CTGATTAAGAAATATAGTATCAGTAACAAAGAAATCTCACATGCGCTGAGGATGTC 390
 QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAspAlaIleSerLys 40
 Db 391 ATTATCTTAAGTCACTCGGAATAAGGGTTTGAAGGTGAGATGATGATCATGATCAACAAA 450
 QY 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuLysArgAsnAsnMetGlnHisIleMet 60

Db 451 CTATGATGACCAAGAGATATATGCGGAGCTCTCATCAGAATTAACATGCAACATATAATG 510
 QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluAsnLysGluAsnThrProArgAsn 80
 Db 511 GGGCCAGTACTCGATTAACTCTGGGGGAAGAAACAAAGAGAACACACCTAGCAAT 570
 QY 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
 Db 571 GTTCTAAACATATCCAGCAAGTATGAATATGCTTAAGCACATCTCGAAGGATATAAAG 630
 QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
 Db 631 AAGCCTCAAAAGAGATTCCTCAAGCCCAAGAAAGTCCAGTAAAAAGCAAAAGCACCTCGT 690
 QY 121 IleLysHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
 Db 691 ATTCACACACAACTTGTACTACCTAAACATCTCTCAAAAGTCAAAATAATCCCCAGTAT 750
 QY 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
 Db 751 TTGAGGCGCAGCGGTTATACAGATCTTCAAGAGAGAGGGGACAAATGATATATCTCTTTC 810
 QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
 Db 811 AGTGGGACCGCCCAACCTTTTAAAGGACATCTCTGGTAAAGAGAGAGCTACTGTCTTGAC 870
 QY 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
 Db 871 CTAGAGCGCAAGATATTTCAACAGGGTTTTCAGGCCCAAGTGAAGCTGAGTACTCAT 930
 QY 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn 220
 Db 931 CTTGACACAAAAAGCCAGGTTTAAATGAGATCCAGAGAGAGAGAAATGTTGGAAAT 990
 QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
 Db 991 ACCATTGGAAGTACTAGGATGAACTGCGAAGAGAGCGAGATCTCTTGTATGTCAGCCTTGA 1050
 QY 241 GluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGly 260
 Db 1051 GAGGCGCAGCAACGATATCATGGGTAGTACCAATTTTAAAGAGAGCTCTCTGGAAGAGAGGA 1110
 QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
 Db 1111 AACAGATGATGCTGCGACCCAAATGCTCACCAAGGAGAGGTTGAGTTTCATTACCT 1170
 QY 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
 Db 1171 CCTGCACCTCAAAAGAGAGAAAGAAAGAGAGGAGTAGTATGATGAGTGAAGTACCAAC 1230
 QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
 Db 1231 TATAATGAATTCCTAAAAATGGCAAGGCGAGTACCAGAAAGGTTGATGATTCATTCTAAT 1290
 QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
 Db 1291 AGGAACCAAGCAACCTTTAAATGAAAAACAAAGGTTTCTTAGTAAGGGCAAAAGTACAGGC 1350
 QY 341 LeuProIleProSerArgGlyLeuAspAsnGluLysLysAsnGluMetAspSerPheAsn 360
 Db 1351 CTGCCCATTCCTCTCTGCTGTTGATAATGAATCAAAACGAAATGGATTCCTTTAAT 1410
 QY 361 GlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
 Db 1411 GGGCCCAAGTATGAGATATAATAACATGCGCAAGAAATATCATATTATGATACCCACAGA 1470
 QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGln 400
 Db 1471 CAAATAAATCTACACGAATAAGGGTATGCCAAGGAAAGGCTCCTGGGGTAGACAA 1530
 QY 401 ProHisSerAsnArgArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420


```

; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2019
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-422-5

Alignment Scores:
Pred. No.: 2,59e-214 Length: 2019
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 10 Gaps: 0

US-09-700-696C-2 (1-430) x US-09-794-422-5 (1-2019)

QY 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
DB 381 CTGATAAAGATATAGTATCATCAACAAAGAGATATCTCAATGGCTCGAGGATGTCA 440

QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAspAlaIleSerLys 40
DB 441 ATTTATCTCACTAAGTCAACTGGGATTAAGGGTTTGGAGTGGAGATGATGCTATCAGCAAA 500

QY 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleAsgAsnMetGlnHisIleMet 60
DB 501 CTACATGACCAAGAGATATGGCCAGCTCTCATCAGAAATAACATGCCACATATATG 560

QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80
DB 561 GGGCCAGTCACTCGCATTAATCTCTGGGGAGAGAAACAAAGAGAACACACACCTAGGAAT 620

QY 81 ValLeuAsnIleLeuProIleSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
DB 621 GTTCTAAACATATCCCAAGATATGAATTAATGCTAAAGCACATCCAGGATATAAAG 680

QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
DB 681 AAGCCTCAAGAGATATCCCAAGCCCAAGAAAGTCCAGTAAAAAGCAAAAGCAACCATCGT 740

QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysIleProSerAsp 140
DB 741 ATTCAACACAACTTACATGACCTTAAACATCTCTCAAAAGTCAAAATAATCCCAAGTAT 800

QY 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
DB 801 TTTGAAGGAGCGGTTATACAGATCTTCAAGAGAGAGGGGCAATGATATATCTCTTTC 860

QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
DB 861 AGTGGGAGCGGCAACCTTTTAAGGACATCTCTGTTAAAGAGAGAGAGTCTGCTCTGAC 920

QY 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
DB 921 CTAGAAGGCAAGATATTAACACAGGGTTTGCAGGCCCAAGTGAAGCTGAGAGTACTCAT 980

QY 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluLysGlyAsn 220
DB 981 CTTGACACAAAAAAGCCAGGTTATATGATGATCCCAAGAGAGAGAGAAATGGTGGAAAT 1040

QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuVal 240
DB 1041 ACCATTGGAACACTAGGATGAACTGGGAAAGAGCCAGATGCTGTTGATGCTGCTGTA 1100

QY 241 GluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGly 260
DB 1101 GAGGGAGCAACGATATCATGGGTAGTACCAATTTTAAGGAGCTCCCTCGAAGAGGA 1160

261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
1161 AACAGAGTGGATGCTGGCAGCCAAATGCTCACCAGGAGAGCTTGAGTTTCATTACCT 1220

QY 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
DB 1221 CTTGCACTCCCTCAAAAGAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1280

QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
DB 1281 TATAATGAATTCCTTAATAATGGCAAGGCACTACCAGAAAGGGTGTAGATCATTTAAT 1340

QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
DB 1341 AGGAACCAAGCAACCTTAATAATGAAACAAAGAGTTTCTTAGTAAGGGCAAAAGTACAGGC 1400

QY 341 LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn 360
DB 1401 CTGCCCATTCCTTCTCTGCTGCTTGTGATATGAATCAAAACGAAATGATTCCTTTAAT 1460

QY 361 GlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
DB 1461 GGCCCCAGTCATGAGATATATAACACATGGCAGAAATATCATTTATGCCCCACAGA 1520

QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGln 400
DB 1521 CAAATATTTCTACAGGATAGGATATGCCACAGGAGGAGAGGCTCTCTGGGGTAGACAA 1580

QY 401 ProHisSerAsnArgPheSerSerArgArgAspAspAspSerSerGluSerSerAsp 420
DB 1581 CCCCATTCCAACAGGAGGTTTAGTTCCTCCGTAGAAGGGATGACAGTAGTAGTCATCTGAC 1640

QY 421 SerGlySerSerSerGluSerAspGlyAsp 430
DB 1641 AGTGGCAGTTCAAGTGAAGGCGGATGGTGAC 1670

RESULT 8
US-09-794-422-7
; Sequence 7, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC1045
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 7
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-794-422-7

Alignment Scores:
Pred. No.: 2,75e-214 Length: 2112
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 10 Gaps: 0

US-09-700-696C-2 (1-430) x US-09-794-422-7 (1-2112)

QY 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
DB 1101 GAGGGAGCAACGATATCATGGGTAGTACCAATTTTAAGGAGCTCCCTCGAAGAGGA 1160

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474 CTGAATAAAGAAATATAGTATCAGTAACAAGAGAAATCTCACAATGCGCTGAGGATGCA 533
QY 21 IletVrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
Db 534 ATTTATCTTAAGTCAACTGGGAATAAAGGGTTTGAGGATGGAGATGATGCTATCAGCAA 593
QY 41 LeuHisAspGlnGluGlyThrGlyAlaAlaLeuIleArgAsnMetGlnHisIleMet 60
Db 594 CTACATGACCAAGAGAAATATGGCGCAGCTCTCATCAGAAATAACATGCAACATATATG 653
QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80
Db 654 GGGCAGTGAAGTGGATTAAGTCTCTGGGGAGAGAAACAAAGAGAGACACACCTAGGAAT 713
QY 81 ValLeuAsnIleLeuProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 714 GTTCTAAACATAATCCCAAGCAAGTATGTAATATGCTAAAGCACACTCGAAGGATAAAG 773
QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 774 AAGCTCTCAAGAGATCCCNAGCCAGAAAGTCCAGTAAAGCAAAAGCAACCATCGT 833
QY 121 IleGlnHisAsnIleAspTyrIleuLysHisIleuSerLysValLysLysIleProSerAsp 140
Db 834 ATTCAACACAACTGACTACCTAAACATCTCTCAAAAGTCAAAAGCAAAATCCCGAGTAT 893
QY 141 PheGluGlySerGlyTyrThrAspLeuGlnArgGlyAspAsnAspIleSerProPhe 160
Db 894 TTGGAAGCAGCGGTATACAGATCTTCAAGAGAGAGGGCAATGATATATCTCTTC 953
QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 954 AGTGGGACGGCAACCTTTTAAGACATCTCTGTTAAAGGAGAGAGCTACTGGTCTGTAC 1013
QY 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 1014 CTGAAAGGCAAGATATTCAACAGGGTTTGAGGCCCAAGTGAAGCTGAGAGTACTCAT 1073
QY 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn 220
Db 1074 CTTGACACAAAAGCGGTATATATGAGATCCCAAGAGAGAGAGAAATGGTGGAAAT 1133
QY 221 ThrIleGlyThrArgAspGlnThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
Db 1134 ACCATTGGAACTAGGATGAACTGCGAAAGAGGAGAGATGCTGTTGATGTCAGCCTTGA 1193
QY 241 GluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGly 260
Db 1194 GAGGGCAGCAACGATATATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 1253
QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyValGluPheHisTyrPro 280
Db 1254 AACAGAGTGATGCTGGCAGCCAAATGCTCAAGAGGAGGAGTATGATGATGATGATGAT 1313
QY 281 ProAlaProSerLysGluLysArgLysGluGlySerAspAlaAlaGluSerThrAsn 300
Db 1314 CTTGACCTCTCAAGAGAAAGAAAGAGAGGAGGAGTATGATGATGATGATGATGATGAT 1373
QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1374 TATAATGAAATCTCTAAATATGCAAGAGGAGGAGTATGATGATGATGATGATGATGAT 1433
QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1434 AGNACCAAGCAACCTTAATGAAACAAAGAGGTTCTTCTAGTAAAGGCAAAAGTCAAGGC 1493
QY 341 LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn 360
Db 1494 CTGCCATCTCTCTGCTGCTTGTATGATGAAATCAAAACCAAAATGAGTATCTTTAAT 1553
QY 361 GlyProSerHisGluAsnIleLeuThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1554 GGCCCCAGTCTATGAGATATATATACATGAGGAGAGAAATATCATTTATGATCCCCACAG 1613

QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGln 400
Db 1614 CAAATAATATTCACACGGAATAAGGTATGCCACAGGGAAGAGCTCTCTGGGTAGACAA 1673
QY 401 ProHisSerAsnArgArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
Db 1674 CCCCATTCCACAGGAGGTTTATGTTCCCGTAGAGGATGACAGTAGTGAATCTCTGAC 1733
QY 421 SerGlySerSerSerGluSerAspGlyAsp 430
Db 1734 AGTGGCAGTTCAAGTGAGAGCGATGGTGAC 1763

RESULT 9

US-09-794-422-3
Sequence 3, Application US/09794422
Publication No. US20030166239A1
GENERAL INFORMATION:
APPLICANT: Brown, Thomas A.
APPLICANT: De Wet, Jeffrey R.
APPLICANT: Gowen, Lori C.
APPLICANT: Hames, Lynn M.
TITLE OF INVENTION: Mammalian Osteoregulins
FILE REFERENCE: PCI0445
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/185,617
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 60/234,500
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 1682
TYPE: DNA
ORGANISM: Mus musculus
US-09-794-422-3

Alignment Scores:
Pred. No.: 3,96e-87 Length: 1682
Score: 983.50 Matches: 217
Percent Similarity: 62.56% Conservative: 52
Best Local Similarity: 50.47% Mismatches: 134
Query Match: 43.15% Indels: 27
DB: 10 Gaps: 8

US-09-700-696C-2 (1-430) x US-09-794-422-3 (1-1682)

QY 6 SerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSerIleTyrProLysSer 25
Db 166 AGCTGGCGCAATCAAGACAGCAATTCACAGGACTTGGCAGCATCTGTGTATCTGTATCCC 225
QY 26 ThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLysLeuHisAspGlnGlu 45
Db 226 ACCTGTGATGAAGCAGAGAGTGGCAAGGTGCTCTCTTCCACCGCTGCCAGGAC 285
QY 46 GluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAla 65
Db 286 AGGTATGGTGTGCTCTCTCTCTCAGAAATATCAGCAGCCTGTAAAGAGTCTAGTACTGGG 345
QY 66 IleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIle 85
Db 346 GCCGAATCTAGGAGGAGAAACACAGGAGAGAGCTCAGAGTGTCTTCTAGGCTAAT 405
QY 86 ProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAsp 105
Db 406 CCAGCAGATGTCATGATGCTTAAAGTCTCTTAAAGACATAAAGATCAAGAGATTAT 465
QY 106 SerGlnAlaGlnLysSerProValLysSer-----LysSerThrHisArgIleGln 122
Db 466 CTGTAAACCCAGAGACCGCGGTCAAAAGCAACACACCAACACACCCCGCAGCCGA 525
QY 123 HisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAspPheGlu 142

Db 526 CGGACCTACTACCTCCACATCTCCACAGATCAAGAGACTCCAGTGGCTTGA 585
Qy 143 GlySerGlyThrAspLeuGlnArgGlyAspAsnAspIleSerProPheSerGly 162
Db 586 GCGAGTGGCTCCCGAGATCTTCTAGTGGGAGAGATATGATGTCCTCCCTTTTTCAGTGA 645
Qy 163 AspGlyGlnProPheLysAspIleProGlyLysGlyGluAla---ThrGlyProAspLeu 181
Db 646 GATGGGCAACATTTTATGCACATCTCTGGCAAGGAGGTGCTGGGTCTGGCTCTGA--- 702
Qy 182 GluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeu 201
Db 703 -----AGCTCAACTAGTGGCCCCCTCTCAGGCTCCAGCAAGCTGAAGTTATTGAACCA 756
Qy 202 AspThrLysLysProGlyTyraAsnGlnProGluArgGluGluAsnGlyGlyAsnThr 221
Db 757 CATATGAGTGGTACTAGGCTCTATAGATCCCGGGAGAGAGACATGTTGGCAGTGC 816
Qy 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
Db 817 TATGCAACAGAGACAAAGCTGCACAGGGGGGAGGCTCTGCAGAGTGGGAGGCTTGTGGGG 876
Qy 242 GlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsn 261
Db 877 GCGAGATGAATCAGAGGAGCACCATTTCAGGGAATCTCCCGGAAAGAGAGAAAC 936
Qy 262 ArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyProPro 281
Db 937 AGAATTAATGCCCGAGCAGCAAAATGCTCATCAAGGAGAAAGTAGAATTTCACTATCCACA 996
Qy 282 AlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsnTy 301
Db 997 GTGGCTTCAGAGAAAGTAAGGGGCGGTGGAGCATGCGAGGAGAGCT---GGTTAC 1053
Qy 302 AsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArg 321
Db 1054 AACGAATCCCCAGAGCAGCAAGTAGCTCTAGCAAGATGTCAGAGAGTCCCAAGGG 1113
Qy 322 AsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeu 341
Db 1114 AACCAATTAACTTGACTCCAGCAGCAAGATTTCCAGGTAAAGGCAGGAGGCGCCT 1173
Qy 342 ProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGly 361
Db 1174 GCTGCTCCCTCTCACAGTCTTAGTAATAGGTTAAAGTGAA----- 1215
Qy 362 ProSerHisGluAsnIleThrHisGlyArgLysTyHisTyValProHisArgGln 381
Db 1216 -----GAAAC-----CATATGTGTCTCATGACAA 1242
Qy 382 AsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTip---GlyArgGln 400
Db 1243 AATAATCTTACCGGATTAAGGATGTCAGCGGAGAGGCTCTGGCCTTCGAGAAGA 1302
Qy 401 ProHisSerAsnArgPheSerSerArgArgAspAspSerGluSerSerAsp 420
Db 1303 CCAATATCCACAGGCGCTAGCACCCGCCAAGA---GACAGAGGAGTGGTCTATCC 1359
Qy 421 SerGlySerSerSerGluSerAspGlyAsp 430
Db 1360 AGTGGAGTTCTAGTGAGAGTCAATGTGTGAC 1389

RESULT 10

US-09-794-422-1
; Sequence 1, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins

FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1655
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-794-422-1

Alignment Scores:
Pred. No.: 1,05e-82 Length: 1655
Score: 938.50 Matches: 211
Percent Similarity: 59.95% Conservative: 45
Best Local Similarity: 49.41% Mismatches: 146
Query Match: 41.18% Indels: 25
DB: Gaps: 8

US-09-700-696C-2 (1-430) x US-09-794-422-1 (1-1655)

Qy 9 AsnLysGluAsnThrHisAsnGlyLeuArgMetSerIleTyProLysSerThrGlyAsn 28
Db 146 AACCAAGGCAACATCCAC-----TTAGCATCTGTGAAGCTGAGCCCATGTTGGGT 196
Qy 29 LysGlyPheGluAspGlyAspAspAlaIleSerLysLeuHisAspGlnGluGlyGly 48
Db 197 AAAGAACAGAGGGTGGGAGATGCTCCCTTACCTGCTTGACCAGAACAGGAGGGT 256
Qy 49 AlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLeu 68
Db 257 GCCACCTCTCTCAGAAATATCATCTCAGCTGTAAAGAGTCTGTGAGGGGACTGAAGTA 316
Qy 69 LeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSer 88
Db 317 CAGAGCGACAGAACAAAGAGAGAAACCTCAGAGTGTCTAAGCGTAATTCACACAGAT 376
Qy 89 MetAsnTyraLysAlaHisSerLysAspLysLysLysProGlnArgAspSerGlnAla 108
Db 377 GTCCACAATACTAACGACTACTCAGAGATACAGAGAACCAACAGAGGGGATCTACTACT 436
Qy 109 GlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyLeu 128
Db 437 CAGAACAGCCAGAGCAAGCAACACACCCCTCGGGCCCGAGAGCAGCAGCTACCTA 496
Qy 129 LysHisLeuSerLysValLysLysLysIleProSerAspPheGluGlySerGlyTyThrAsp 148
Db 497 ACACATCTCCCCAAATCAGAAAGATTCTCAGTGACTTCGAGGACAGTGTCTCCCGAGAC 556
Qy 149 LeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLys 168
Db 557 CTTCAGTGGGGGGGATATGATGTCCTCTTTCAGTGGAGATGGACACACATTTATG 616
Qy 169 AspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu-----GlyLysAsp 185
Db 617 CACACTCCGACAGAGAGGTGCTGTGGATCTGATCTGAAAGCTCAGTGTGTCCACCT 676
Qy 186 IleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspThrLysLys 205
Db 677 GTG-----TCAGGCTCCAGCAATGTCAGATTGTTGACCCACACAGCAATGGA 724
Qy 206 ProGlyTyraAsnGluIleProGluArgGluGluAsnGlyLysIleGlyThrArg 225
Db 725 CTGGGCTTAATGAGATCCCGAGGAGAGAGGTCACATAGGCGGTGCTATGCAACCCAGA 784
Qy 226 AspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySerAsnAsp 245
Db 785 GGAATAACTGCGAGGGGCGAGGTTCGCGGATGTGAGCCTTGTGGAGGCGAGCAATGAA 844

QY 246 IleMetGlySerThrAsnPhelysGluLeuProGlyArgGluGlyAsnArgValaspala 265
 DB ATCCGGCGAGTACCAAAATTTAGGAGCTCCCTGGAAAAGAGGAAACAGAGTCGATGCC 904
 QY 266 GlySerGlnAsnAlaHisGlnGlyValGluPheHisTyrProAlaProSerLys 285
 DB AGCAGGCAAAATGCTCATCAGGAAAGTAGATTTCTACTCCCAAGCGCCCTCAAAA 964
 QY 286 GluLysArgGlyGluSerSerAspAlaAgluSerThrAsnTyrAsnGluLeuPro 305
 DB GAGAGGTAAGAGGGGCGCAGCAGGAGCACACAGGGAAGCGGTACAATGAAATCCCC 1024
 QY 306 LysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnAsnGlnAlaThr 325
 DB AAGAGCAGCAGAGCGCGCTAGCAAGATGCGGAAGATCTAAAGGGAACCAAGTAACC 1084
 QY 326 LeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProfileProSer 345
 DB TTGACTGAAAGCCAAAGGTTCCAGGCAAAAGGCAAGGCCAGTCT-----TCT 1132
 QY 346 ArgGlyLeuAspAsnGluLeuLysAsnGluMetAspSerPheAsnGlyProSerHisGlu 365
 DB 1133 CACAGTCTTGATGAGGTAAAGTGAAGAGACTCTTCTAATAGTCTCAGTAGAGAG 1192
 QY 366 AsnIle---IleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSer 384
 DB 1193 GGGATTGCAATACACACAGGAGAACAGCCAC-----CCT 1228
 QY 385 ThrArgAsnLysGlyMetProGlnGlyLysGlySerTyr---GlyArgGlnProHisSer 403
 DB 1229 ACACGAATAGGGGATGTCACAGCGAGAGGCTCTCGGCTCGAGAGACCCCATCCC 1288
 QY 404 AsnArgArgPheSerSerArgArgAspAspSerSerGluSerSerAspSerGlySer 423
 DB 1289 CACCGCGCGTAGCACCCGCCAAGA---GACAGTAGTGTATCATCATCCAGTGGAGT 1345
 QY 424 SerSerGluSerAspGlyAsp 430
 DB 1346 TCTAGCAGAGCAGTGGTGAC 1366

RESULT 11

; Sequence 39715, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 39715
 ; LENGTH: 1189
 ; TYPE: DNA
 ; ORGANISM: Xanthomonas campestris
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)...(1189)
 ; OTHER INFORMATION: unsure at all n locations
 ; US-10-369-493-39715

Alignment Scores:

Pred. No.: 3,43e-05 Length: 1189
 Score: 149.50 Matches: 91
 Percent Similarity: 36.16% Conservative: 41
 Best Local Similarity: 24.93% Mismatches: 143

Query Match: 6.56% Indels: 90
 DB: 15 Gaps: 20
 US-09-700-696C-2 (1-430) x US-10-369-493-39715 (1-1189)
 QY 70 GlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSerMet 89
 DB 252 GGGAAATAACCGAAAGAACCCACC----- 275
 QY 90 AsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAlaGln 109
 DB 276 -----GCGAAGAACACAGACCCCGAGCGCCACAGGAGCAACCAACACAA 329
 QY 110 LysSerProValLysSerLysSerThrHisArgLysGlnHisAsnIleAspTyrLeuLys 129
 DB 330 ACCCGGACACAAAGAGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCGCCCG 389
 QY 130 HisLeu-----SerLysValLysLysLysLysLysLysLysLysLysLys 444
 DB 390 AAAAAAGGGGGAACGGGGAACACAGAGTGAACAAACAAACCGCAGAAAAACAGAGA 449
 QY 145 GlyTyrThrAspLeuGln-GluArg-----GlyAspAsnAspLysSerProPh 160
 DB 450 AGACACACAAAGAGAGAGAGACGACGACAAAGCAAGCGGCGGAGAGAGAGCGCCCG 509
 QY 160 eSerGlyAspGlyGln-----ProPheLysAsp---IleProGlyLysGlyGlu 176
 DB 510 GGGAGGGGAAGAAACACACAGCCACCCCGGAGGAGGAGAACCGCGGGGCACACCGAAC 569
 QY 176 aThrGlyProAspLeuGluGlyLysAspLysLysLysLysLysLysLysLysLys 196
 DB 570 AACC-----CAAGAGGGAAGGAATGAAAGAAC-----ACAGGACCAAGACCGC 614
 QY 196 aGluSerThrHisLeuAspThrLysLysProGlyTyrAsnGluLysLysLysLys 216
 DB 615 GACGGGCAACACCGACCAAGAAACCGGAGGA-----GACCAACCCCAACAAACAA 668
 QY 216 uAsnGlyGlyAsn-----ThrIleGlyThrArgAspG 227
 DB 669 A-----GGGAACGAGACAAAGCGCGCGCGATAGACAGAAACGAAACCGACCA 722
 QY 227 uThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySerAsnAspIle 247
 DB 723 AACAGGAGCGAAGGAGCGCA-----CGAAACAAACCCACCGCACCT 764
 QY 247 tGlySerThrAsnPhelysGluLeuProGlyArgGluGlyAsnArgValaspala 267
 DB 765 CGGACACACAGAGCGCGCAGAA---AAGCAAGAGAGAGGCAACCGACGAAACCGGGGA 819
 QY 267 rGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro----- 280
 DB 820 -----GGGCACCCCAACAGCAACACGACAGACCCCGGACGAGAGGAGCAGAGA 872
 QY 281 -ProAlaProSerLysGlyLysArgLysGlyLysSerAspAlaLysLysThrAs 300
 DB 873 GAAACCCGACGCGGAGAGGAGACAGAGAAACAAACAAAGAAACCAACGACGAGAG 932
 QY 300 nTyrAsnGluLeu-----ProLysAsn-----GlyLysGlySerThrArg 314
 DB 933 AGAGAACGAGATACCGGAGCAGCAGAGAAACAAACCCCGAGGAGGAGGAGCGGC 992
 QY 314 sGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPhePro 334
 DB 993 ACGGGAAGAACACACAGAGAGGAGCAACCGCGCAGCGGCAAC-----CCGAA 1037
 QY 334 rLysGlyLysSerGlnGlyLeuProLysLysLysLysLysLysLysLysLysLys 354
 DB 1038 CCGAGGGAAGCGACCC-----GACAAAGGGGCGCAAGG 1070
 QY 354 nGluMetAspSerPheAsnGlyProSerHisGluAsnIleIleThrHisGlyArgLys 374
 DB 1071 ACAGACCGGGAACACACACAGACACAGCAGG-----AGGGGACCGCAGAA 1118

QY 374 rHisTyrValProHisArgGlnAsnSerThrArgAsnLysGlyMetProGlnGlyLy 394
 Db 1119 CACACCAAG-----CAGCAGACGGAGCGCGGAGCAACACACACCGGAGCG 1169
 QY 394 sGlySerTrpGly 398
 Db 1170 AGGAGCAAGGC 1182

RESULT 12

US-10-363-798-1
 ; Sequence 1, Application US/10363798
 ; Publication No. US20030180280A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kong, Xiangyin
 ; APPLICANT: Xiao, Shuangxi
 ; APPLICANT: Zhao, Guoping
 ; APPLICANT: Yu, Chuan
 ; APPLICANT: Hu, Landian
 ; TITLE OF INVENTION: METHOD OF DIAGNOSING AND TREATING DENTINOGENESIS IMPERFECTA
 ; TITLE OF INVENTION: TYPE II USING DENTIN SIALOPHOSPHOPROTEIN GENE AND CODED
 ; FILE OF INVENTION: PRODUCT THEREOF
 ; FILE REFERENCE: 9548.78USWO
 ; CURRENT APPLICATION NUMBER: US/10/363,798
 ; CURRENT FILING DATE: 2003-03-05
 ; PRIOR APPLICATION NUMBER: CN 00125042.6
 ; PRIOR FILING DATE: 2000-09-05
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 8201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-363-798-1

Alignment Scores:

Pred. No.: 0.000536 Length: 8201
 Score: 148.50 Matches: 92
 Percent Similarity: 38.43% Conservative: 84
 Best Local Similarity: 20.09% Mismatches: 218
 Query Match: 6.52% Indels: 64
 DB: 14 Gaps: 14

US-09-700-696c-2 (1-430) x US-10-363-798-1 (1-8201)

QY 4 GluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeu-ArgMetSerIleTyrPr 23
 Db 5214 AAATATTCATAGTTAATCATCTTTCTCCATCCTTCCATAGGGAATAGAAATCAAGG 5273
 QY 23 oLysSerThrGlyAsnLysGlyPhe-----GluAspGlyAspAspAlaIleSerLysLe 41
 Db 5274 TCCACGACGTGGCAACAGAAATATTACCAAGAGTTGGGAAAGCAACGAAAGTTAA-- 5331
 QY 41 uHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGl 61
 Db 5332 -GAGGATAAGGACAACATGGAATGATCTTGGCAAGCAATGTCAAG---ACACAAGG 5387
 QY 61 yProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsnVa 81
 Db 5388 AGAGGTGTTCACATAGAGACCTGCCCAAAATCAGAA-----CCAGGAATATA 5438
 QY 81 lLeu-----AsnIl 84
 Db 5439 AGTTGGACACAGCAATACAGGTAGTGACCAATAGTGTGATGATGACAGTTATGATT 5498
 QY 84 eIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnAr 104
 Db 5499 TGATGATAGTCCATCCAGGAGATGATCCCATAGCAGTGTGATCTAATGGCAATGA 5558
 QY 104 gAspSerGlnAlaGlnLysSerProValLysSerThrHisArgIleGlnHis 124
 Db 5559 TGATGCTAATTCAGAA---AGTGACAATAACAGCAGTACCGAGGAGATGCTTCTTATAA 5615
 QY 124 nIleAspTyrLeuLysHisLeuSerLysValLysIleProSerAspPheGluGlySe 144

Db 5616 CTCTGATGAA-----TCAAAAGATAATGCAATGCGAGTGTCTCAAAAGAGGC 5663
 QY 144 rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164
 Db 5664 AGAAGATGATGACAGTGTAGCAGCATATCACTAATAATAGTACAGTAATGGCAATGG 5723
 QY 164 yGlnProPheLysAsp-----lLeProGlyLysGlyGluAlaThrGlyPr 179
 Db 5724 TAACATGGGAATGATGACAATGACAATCAGACAGTGGCAAAAGGTAAATCAGATAGCAG 5783
 QY 179 oAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerTh 199
 Db 5784 TGACAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 5843
 QY 199 rHisLeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGl 219
 Db 5844 CACAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 5903
 QY 219 yAsnThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLe 239
 Db 5904 CAGTGTAGTGTAGTGTAGTGTAT---AGCAGCAATAGCAGTGTAGTGTAGTGTAGTGA 5960
 QY 239 uValGluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArg-- 258
 Db 5961 TAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 6020
 QY 259 -----GluGlyAsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGl 276
 Db 6021 AGAGAGCGACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 6080
 QY 276 uPheHisTyrProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAl 296
 Db 6081 CAGTGTGTGACACAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 6140
 QY 296 aGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyVa 316
 Db 6141 TGACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 6195
 QY 316 lAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGl 336
 Db 6196 -GACAGCAACACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 6254
 QY 336 yLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMe 356
 Db 6255 CAGTGTAGT-----AGTGACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 6299
 QY 356 tAspSerPheAsnGlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTy 376
 Db 6300 TGACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 6330
 QY 376 rValProHisArgGlnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySe 396
 Db 6331 -----GACAGCAGCAACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 6380
 QY 396 rTrpGlyArgGlnProHisSerAsnArgPheSerSerArgArgAsp----- 413
 Db 6381 CAGCAACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 6440
 QY 414 -----AspSerSerClusSerSerAspSerGlySerSerSerGluSerAsp 428
 Db 6441 TAGCAGTGTAGCAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGAAC 6492

RESULT 13

US-10-108-260A-1338
 ; Sequence 1338, Application US/10108260A
 ; Publication No. US20040005560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
 ; FILE REFERENCE: HI-A0106
 ; CURRENT APPLICATION NUMBER: US/10/108,260A
 ; CURRENT FILING DATE: 2002-03-27

; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1338
; LENGTH: 3045
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-1338

Alignment Scores:
Pred. No.: 0.000165 Length: 3045
Score: 148.00 Matches: 106
Percent Similarity: 34.76% Conservative: 65
Best Local Similarity: 21.54% Mismatches: 209
Query Match: 6.49% Indels: 112
DB: 15 Gaps: 24

US-09-700-696C-2 (1-430) x US-10-108-260A-1338 (1-3045)

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QY 1 ValAsnLysGluTyrSerIleSerAsnLys-----GluAsnThrHisAsnGly 16
Db 119 GTAAACGCGAAGCATCACATTAAAGGAAAGAGGGAGTTCAGGAATCCAGAGGGGC 178
QY 17 Leu-----ArgMetSerIleTyrPro 23
Db 179 CTGGTACAGATGAGACAGATTTAGAGGATGAAATCAAGAGGCGATGCTGCGACAGT 238
QY 24 LysSerThrGlyAsnLys-----GlyPheGluAspGlyAspAlaIle 38
Db 239 TCTGTTTACAGCAATAACCTCAACTCTATGCCAGCTGCTGAAAGGGTAAAGACACATTA 298
QY 39 SerLysLeuHisAspGlnGluGlu-----TyrGlyAlaAlaLeu-----IleArgAsn 54
Db 299 AATATCAGCTATATGATACAGAAATGACCTAAAGAGGAGCAGCTATTCTATCTCMAAA 358
QY 55 AsnMetGlnHisIleMetGlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLys 74
Db 359 GGAATGCTCCACGAAGAAAGCCCTGGAGAGCAGCATTTTGAAGGTGGCTCAGAGATGAA 418
QY 75 -----GluAsnThrProArgAsnValLeuAsn-----IleIleProAlaSerMet 89
Db 419 TCTGCACGAAAGCTGCAGGAGATCAATGAAATGACAGAAAGATTCAACAGGAAATCCCTG 478
QY 90 AsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAlaGln 109
Db 479 GGTAGTGCACCACTCATGGAGATGACCACTTAAGCATCCAGACAGATGTGGAGGGA 538
QY 110 LysSerProValLysSerLysSerThrHis-----ArgIleGlnHisAsnIleAspTyr 127
Db 539 GACCTTTGTTAAATGGGGCCAACTGCACACGCTTTCAGTGGAGCATCACTGAGGAA 598
QY 128 LeuLysHis-----LeuSerLysValLysLysIleProSerAspPheGluGlySerGly 145
Db 599 TTGAAGAGGAAATAGTTCTTAAACTCAAAACCAACCTAGA---TTCTCTCTCCAGAT 655
QY 146 TyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGln 165
Db 656 GAGATTGATTGGCCAGAGAACTCGAAGACGAGGTT---CCCATTTCTGGGAAGAAATCTT 712
QY 166 ProPhe-----LysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
Db 713 CCCTGGCAACAAGAAAGAGATGTG-----GCTGCCACAGCCAGCAAGCAATG 760
QY 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAsp 202
Db 761 AGTGAGAAGATPAAG-----CTCTCTGAGGGAAGCAAGCAAGAGGACTCCTTGGAT 811
QY 203 ThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIle 222
Db 812 -----GAAGAGTTTTTTCATCACAGGCAATGCGAGGCGCACAGAGGTA 853
QY 223 GlyThrArgAspGluThr-----AlaLysGlu 231
Db 854 GGACAGACAGACCAACTGACAGCAGAGGAGGACAGCTTTCTTTCTTAAGTAGAAGAG 913
```

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QY 232 AlaAspAlaValAspValSerLeuValGluGlySerAsnAspIleMetGlySerThrAsn 251
Db 914 GATGATATATCCCTCTGAGAGACTTAGAGGATGAAACGCTATAAATGCAAAACGGTCT 973
QY 252 PheLysGluLeuProGlyArgGluGlyAsnArgValAspAlaGlySerGln-----268
Db 974 AAAGAAAAAACCCGGGAATCAGGCGCAGCTTTGATGTTGATCTGCAAGTCCCTGAC 1033
QY 269 AsnAlaHisGlnGlyLysValGluPheHisTy-ProProAlaProSerLysGluLysArg 288
Db 1034 AGACGATTTTAGGACCATTCAT-----CCAGATCCAGAAATTTGAAGAAAGC 1081
QY 289 LysGluGlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGly 308
Db 1082 AAGCAAGAAACTAGTATGATTTTGGATAGTGAAGAAACAAAGTGAG-----1126
QY 309 LysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGlu 328
Db 1127 -----ACTGCTGCCAAGGGTCAACACAGGAGGCGGACCAAAATACATGGTGGAA 1180
QY 329 LysGlnArg-----PheProSerLysGlyLysSer 338
Db 1181 AAAGACGCGCTTGGCAGATAAGAAAGCACAGAGACCATTTGACGAAAGTGACTTTTCT 1240
QY 339 GlnGlyLeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSer 358
Db 1241 GACAGATAAAATTCAGACTCCAGANTTAGGTGAGTGTTCAGATTAAGATTCTTGAT 1300
QY 359 Phe-----AsnGlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyr 376
Db 1301 TATCTGAAGAACGACCAACCTCTGAGGAACATCTGAAGACCTCAGGGCTT-----1348
QY 377 ValProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer 396
Db 1349 -----GCAGGGGAGCTGTGAGGAGAACTCTCA 1375
QY 397 TrpGlyArgGlnProHisSerAsnArgArgPheSerSerArgArgAspAspSerSer 416
Db 1376 -----AAAGAGCAGCATGAGAAC-----ACAGAGAGAGTACATGGGCACA 1414
QY 417 GluSerSerAspSerGlySerSerSerGluSerAsp 428
Db 1415 GAAGACCGAGGGTCTGTCTGTGCAGAAACCTGAAGAT 1450
```

RESULT 14
US-10-210-172-65
; Sequence 65, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shinkets, Richard
; APPLICANT: Zerkusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Vernet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalte, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly

; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Malyankar, Uriel
 ; APPLICANT: MacDougall, John
 ; APPLICANT: Stone, David
 ; APPLICANT: Alsobrook II, John
 ; APPLICANT: Lepley, Denise et al.
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
 ; FILE REFERENCE: 21402-416 A US/10/210,172
 ; CURRENT APPLICATION NUMBER: 2001-08-01
 ; PRIOR FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: 60/309,501
 ; PRIOR FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/323,994
 ; PRIOR FILING DATE: 2001-09-21
 ; PRIOR APPLICATION NUMBER: 60/373,814
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/310,291
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: 60/310,951
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/310,544
 ; PRIOR FILING DATE: 2001-08-07
 ; PRIOR APPLICATION NUMBER: 60/311,292
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 60/311,979
 ; PRIOR FILING DATE: 2001-08-13
 ; PRIOR APPLICATION NUMBER: 60/313,201
 ; PRIOR FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: 60/312,892
 ; PRIOR FILING DATE: 2001-08-16

; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 327
 ; SOFTWARE: Curaseq! version 0.1
 ; SEQ ID NO 65
 ; LENGTH: 4985
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (13)..(4785)
 ; US-10-210-172-65

Alignment Scores:
 Pred. No.: 0.000314 Length: 4985
 Score: 148.00 Matches: 106
 Percent Similarity: 34.76% Conservative: 65
 Best Local Similarity: 21.54% Mismatches: 209
 Query Match: 6.49% Indels: 112
 DB: 12 Gaps: 24

US-09-700-696C-2 (1-430) x US-10-210-172-65 (1-4985)

QY 1 ValAsnLysGluTyrSerLeuSerAsnLys-----GluAsnThrHisAsnGly 16
 DB 1384 GTAAAGCGAAGACATCACATTAAAGGAAAGGGAGGGAGTTCCAGGAATCCAGAGGGGC 1443
 QY 17 Leu-----ArgMet-SerIleTyrPro 23
 DB 1444 CTGGTACAAGATAAGACAGAAATTAGAGGTGAAATCAAGAAGGCGATGCTGTCACAGT 1503
 QY 24 LysSerThrGlyAsnLys-----GlyPheGluAspGlyAspAlaIle 38
 DB 1504 TCTGTTCCACAGCAATAAACCCTCACTCTATGCCAGCTGCTGAAAGGGTAAAGACACATTA 1563
 QY 39 SerLysLeuHisAspGlnGlu-----TyrGlyAlaAlaLeu-----IleArgAsn 54
 DB 1564 AATACAGCTTATGATGATACAGAAATGACCTTAAAGAGGAGCGATTCATATCTCAAAA 1623
 QY 55 AsnMetGlnHisIleMetGlyProValThrAlaIleLysLeuGlyGluGluAsnLys 74
 DB 1624 GGAATGCTCCACGAGAAAGCCCTGGAGAGCAGATTTTGGAGGGTGGCTCAGAGAGTGAA 1683

QY 75 -----GluAsnThrProArgAsnValLeuAsn-----IleIleProAlaSerMet 89
 DB 1684 TCTGCACAGAAAGCTGCAGGGAATCAATGAATGACAGAAAGATTCAACAGGAATCCCTG 1743
 QY 90 AsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAlaGln 109
 DB 1744 GGTAGTCACCACTCATCTGGAGATGACCCCTAACGCATCCAGACAGACAGTGTGGAGGA 1803
 QY 110 LysSerProValLysSerLysSerThrHis-----ArgIleGlnHisAsnIleAspTyr 127
 DB 1804 GAGCTTTGGTAAATGGGCCAACTGCACACACCTTCAGTGGAGCATCACTGTAGGAA 1863
 QY 128 LeuLysHis-----LeuSerLysValLysLysIleProSerAspPheGluGlySerGly 145
 DB 1864 TTGAACAGAGGAATTAGTTCTTAAACTCAAAACCAACTAGA--TTCTCCTCTCCAGAT 1920
 QY 146 TyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGln 165
 DB 1921 GAGATTGATTTGCCAGAGAACTGGAGACAGCGTT---CCCATCTCTGGGAGAAATCTTT 1977
 QY 166 ProPhe-----LysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
 DB 1978 CCTGGCAACAAGAAAGAGATGTG-----GCTGCCACACCCAGTAACCAATG 2025
 QY 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAsp 202
 DB 2026 AGTGAGAGAGATAAG-----CTCTCTGAGGAGAGCAAGCAAGAGGAGCTCCTTGAT 2076
 QY 203 ThrLysLysProGlyTyrAsnGluIleProGluArgGluAsnGlyGlyAsnThrIle 222
 DB 2077 -----GAAGAGTTTTTCATCACAGCAATGCGGGCAGACAGAGTA 2118
 QY 223 GlyThrArgAspGluThr-----AlaLysGlu 231
 DB 2119 GGACAGACAGACCAAACTGACAGCAGGAGGACCACTTCTCCTTTCTAAAGTAGAAGAG 2178
 QY 232 AlaAspAlaValAspValSerLeuValGluGlySerAsnAspIleMetGlySerThrAsn 251
 DB 2179 GATGATTATCCTCTGAGAACTACTAGAGGATGAAACCGCTATTAATGCAAAACGGTCT 2238
 QY 252 PheLysGluLeuProGlyArgGlyGlyAsnArgValAspAlaGlySerGln----- 268
 DB 2239 AAGAAAAAAACCTCGGAATCAGGCGAGGAGCTTTGATGTTTAACTCTGCAAGTCCCTGAC 2298
 QY 269 AsnAlaHisGlnGlyLysValGluPheHisTyrProProAlaProSerLysGlyLysArg 288
 DB 2299 AGACGAGTTTTAGGCGACCATTCAT-----CCAGATCCAGAAATGAAGAAAGC 2346
 QY 289 LysGluGlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGly 308
 DB 2347 AAGCAAGAACTAGTATGATTTTGGATAGCGAAAAAACAAGTCAG----- 2391
 QY 309 LysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGlu 328
 DB 2392 -----ACTGCTGCAAAAGGGTCAACACAGGAGGCGGAGCAACCAATAACAATGGTGGAA 2445
 QY 329 LysGlnArg-----PheProSerLysGlyLysSer 338
 DB 2446 AAGAAGCGCCTCTGCAGATAAGAAGCACAGACGACCATTTGAACGAGTGACTTTTCT 2505
 QY 339 GlnGlyLeuProLysProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSer 358
 DB 2506 GACAGCATAAAATTCAGATCCAGATTAAGTGAAGTGTTCAGATAAAGATTCATGAT 2565
 QY 359 Phe-----AsnGlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyr 376
 DB 2566 TATCTGAAGAACCAACACCTCTGAGGAACATCTGAAGACCTCAGGGCTT----- 2613
 QY 377 ValProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer 396
 DB 2614 -----GCAGGGGAGGCTGAGGAGAACTCTCA 2640
 QY 397 TrpGlyArgGlnProHisSerAsnArgArgPheSerSerArgArgAspAspSerSer 416

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Db 2641 -----AAAGAGACCATGAGAC-----ACAGAGAGTACATGGGCACA 2679
Qy 417 GluSerSerAspSerGlySerSerGluSerAsp 428
Db 2680 GAAAGCCAGGGGTCTGCTGCTGCAGAACCTGAAGAT 2715

RESULT 15
US-09-785-770A-15
; Sequence 15, Application US/09785770A
; Patent No. US20020103360A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334-328001
; CURRENT APPLICATION NUMBER: US/09/785,770A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/387,462
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 09/145,056
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 4.0
; SEQ ID NO 15
; LENGTH: 5721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(5721)
US-09-785-770A-15

Alignment Scores:
Pred. No.: 0.000375 Length: 5721
Score: 148.00 Matches: 106
Percent Similarity: 34.76% Conservative: 65
Best Local Similarity: 21.54% Mismatches: 209
Query Match: 6.49% Indels: 112
DB: 9 Gaps: 24

US-09-700-696C-2 (1-430) x US-09-785-770A-15 (1-5721)
Qy 1 ValAsnLysGluTyrSerIleSerAsnLys-----GluAsnThrHisAsnGly 16
Db 1372 GTAAACCAGAACATCATATTAAGGAAGGGGGAGTTCCAGGAATCCAAGAGGGGC 1431
Qy 17 Leu-----ArgMetSerIleTyrPro 23
Db 1432 CTGGTACAGATGAGACAGAAATTAGAGGATGAAATCAAGAGGCGATGACTGTGCACAGT 1491
Qy 24 LysSerThrGlyAsnLys-----GlyPheGluAspGlyAspAlaIle 38
Db 1492 TCTGTTTACAGCATATACCTCAACTCTATGCCAGCTGCTGAAAGGGTAAGACATTA 1551
Qy 39 SerLysLeuHisAspGlnGlu-----TyrGlyAlaAlaLeu-----IleArgAsn 54
Db 1552 AAATCAGCTTATGATGATACAGAAATGACCTAAAGAGGACGCTATTATATCTCAAAA 1611
Qy 55 AsnMetGlnHisIleMetGlyProValThrAlaIleLysLeuGluGluAsnLys 74
Db 1612 GGAATGCTCCAGNAGAAAGCCCTGGAGACAGATTTTGAAGGTGGCTCAGAGAGTGAA 1671
Qy 75 -----GluAsnThrProArgValLeuAsn-----IleIleProAlaSerMet 89
Db 1672 TCTGCACAGAAAGCTGCGAGGGAATCAATGAATGACAGAAAGATTCAACAGGAATCCCTG 1731
Qy 90 AsnTyrAlaLysAlaHisSerLysAspLysLysLysProGlnArgAspSerGlnAlaGln 109
Db 1732 GGTAGTCACCATCTATGAGGAGATGACCAACCTTAACGATCCAGACAGACATGTGGAGGGA 1791
Qy 110 LysSerProValLysSerLysSerThrHis-----ArgIleGlnHisAsnIleAspTyr 127

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Search completed: March 29, 2004, 04:28:42

Job time : 530 secs